GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 14:22:04 ; Search time 13.9091 Seconds
(without alignments)
264.899 Million cell updates/sec

Title: US-09-856-803-5
Perfect score: 15
Sequence: 1 gtccgcccgctgagg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	230	4	US-09-437-457-8	Sequence 8, Appli
c	2	14	93.3	6153	2	US-08-347-594A-1	Sequence 1, Appli
c	3	14	93.3	6153	3	US-08-463-682-2	Sequence 2, Appli
	4	13.4	89.3	5434	2	US-08-841-349-1	Sequence 1, Appli
	5	13	86.7	67	1	US-07-977-284A-248	Sequence 248, App
	6	13	86.7	67	2	US-08-256-426B-248	Sequence 248, App
	7	13	86.7	695	2	US-08-403-852D-7	Sequence 7, Appli
	8	13	86.7	695	3	US-08-510-646B-7	Sequence 7, Appli
	9	13	86.7	695	4	US-09-231-818-7	Sequence 7, Appli
c	10	12.4	82.7	425	3	US-08-651-136C-25	Sequence 25, Appl
c	11	12.4	82.7	874	3	US-08-478-507-12	Sequence 12, Appl
c	12	12.4	82.7	874	4	US-09-128-275A-12	Sequence 12, Appl
	13	12.4	82.7	1100	4	US-08-456-200B-17	Sequence 17, Appl
c	14	12.4	82.7	1295	3	US-08-478-507-1	Sequence 1, Appli
	15	12.4	82.7	1295	3	US-08-478-507-5	Sequence 5, Appli
c	16	12.4	82.7	1295	4	US-09-128-275A-1	Sequence 1, Appli
	17	12.4	82.7	1295	4	US-09-128-275A-5	Sequence 5, Appli
c	18	12.4	82.7	1434	2	US-09-055-097-2	Sequence 2, Appli
	19	12.4	82.7	1689	4	US-09-311-924-1	Sequence 1, Appli
	20	12.4	82.7	1735	1	US-08-102-863-10	Sequence 10, Appl
	21	12.4	82.7	1735	5	PCT-US92-10885-10	Sequence 10, Appl
	22	12.4	82.7	1973	4	US-09-311-924-3	Sequence 3, Appli
	23	12.4	82.7	2156	2	US-08-959-011-2	Sequence 2, Appli
	24	12.4	82.7	2303	2	US-08-480-229C-9	Sequence 9, Appli
	25	12.4	82.7	2303	2	US-08-659-235C-9	Sequence 9, Appli
	26	12.4	82.7	2308	2	US-08-480-229C-28	Sequence 28, Appl
	27	12.4	82.7	2308	2	US-08-659-235C-28	Sequence 28, Appl
c	28	12.4	82.7	2336	1	US-08-247-946A-1	Sequence 1, Appli
c	29	12.4	82.7	2336	5	PCT-US95-06420-1	Sequence 1, Appli
	30	12.4	82.7	2470	1	US-07-745-206A-14	Sequence 14, Appl
	31	12.4	82.7	2470	2	US-08-311-363-14	Sequence 14, Appl
	32	12.4	82.7	2793	4	US-09-173-914-35	Sequence 35, Appl
	33	12.4	82.7	3761	4	US-08-890-865A-2	Sequence 2, Appli
	34	12.4	82.7	4173	4	US-08-981-729-9	Sequence 9, Appli
	35	12.4	82.7	4173	4	US-08-981-446B-2	Sequence 2, Appli
	36	12.4	82.7	4522	5	PCT-US93-06251-22	Sequence 22, Appl
	37	12.4	82.7	4843	3	US-08-986-485-1	Sequence 1, Appli
	38	12.4	82.7	5467	1	US-07-745-206A-12	Sequence 12, Appl
	39	12.4	82.7	5467	2	US-08-311-363-12	Sequence 12, Appl
	40	12.4	82.7	6078	4	US-09-173-914-1	Sequence 1, Appli
	41	12.4	82.7	6232	4	US-08-456-200B-11	Sequence 11, Appl
c	42	12.4	82.7	6803	3	US-08-665-259-19	Sequence 19, Appl
c	43	12.4	82.7	6803	3	US-08-762-500-19	Sequence 19, Appl
	44	12.4	82.7	7175	1	US-08-455-543A-8	Sequence 8, Appli
	45	12.4	82.7	7175	2	US-08-193-078B-8	Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-09-437-457-8
; Sequence 8, Application US/09437457
; Patent No. 6273893
; GENERAL INFORMATION:
;  APPLICANT: Giordano, Anthony
;  APPLICANT: Xavier, Ashish
;  TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND METHODS FOR
;  TITLE OF INVENTION: IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
;  TITLE OF INVENTION: INTERACTIONS AND MRNA FUNCTIONALITY
;  FILE REFERENCE: 50093/014001
;  CURRENT APPLICATION NUMBER: US/09/437,457
;  CURRENT FILING DATE: 1999-11-10
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 230
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-437-457-8

  Query Match             100.0%;  Score 15;  DB 4;  Length 230;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db     166 GTCCGCCCGCTGAGG 180


RESULT 2
US-08-347-594A-1/c
; Sequence 1, Application US/08347594A
; Patent No. 5849536
;  GENERAL INFORMATION:
;    APPLICANT:  Garfinkel, Leonard
;    APPLICANT:  Richter, Tamar
;    TITLE OF INVENTION:  CLONING AND PRODUCTION OF HUMAN VON
;    TITLE OF INVENTION:  WILLEBRAND FACTOR GPIb BINDING DOMAIN POLYPEPTIDES AND
;    TITLE OF INVENTION:  METHODS OF USING SAME
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John P. White
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/347,594A
;       FILING DATE:  No. 5849536ember 30, 1994
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  White, John P.
;       REGISTRATION NUMBER:  28,678
;       REFERENCE/DOCKET NUMBER:  36537-B2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-278-0400
;       TELEFAX:  212-391-0525
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6153 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..6153
US-08-347-594A-1

  Query Match             93.3%;  Score 14;  DB 2;  Length 6153;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCGCCCGCTGAGG 15
          ||||||||||||||
Db   4573 TCCGCCCGCTGAGG 4560


RESULT 3
US-08-463-682-2/c
; Sequence 2, Application US/08463682
; Patent No. 6008193
;  GENERAL INFORMATION:
;    APPLICANT:  Leonard Garfinkel, et al.
;    TITLE OF INVENTION:  Cloning and Production of Human Von
;    TITLE OF INVENTION:  Willebrand Factor GPIb Binding Domain Polypeptides and
;    TITLE OF INVENTION:  Methods of Using Same
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  1185 Avenue of Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,682
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  36537-B2-Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6153 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..6153
US-08-463-682-2

  Query Match             93.3%;  Score 14;  DB 3;  Length 6153;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCGCCCGCTGAGG 15
          ||||||||||||||
Db   4573 TCCGCCCGCTGAGG 4560


RESULT 4
US-08-841-349-1
; Sequence 1, Application US/08841349B
; Patent No. 5955594
; GENERAL INFORMATION:
;  APPLICANT: MISHRA, LOPA
;  TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . .
;  FILE REFERENCE: XX/PO4470US0
;  CURRENT APPLICATION NUMBER: US/08/841,349B
;  CURRENT FILING DATE: 1997-04-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 5434
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: For all n's in this sequence, n=(a or g or c or t)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1674)..(2069)
US-08-841-349-1

  Query Match             89.3%;  Score 13.4;  DB 2;  Length 5434;
  Best Local Similarity   93.3%;  Pred. No. 1.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||| ||
Db   1421 GTCCGCCCGCTGCGG 1435


RESULT 5
US-07-977-284A-248
; Sequence 248, Application US/07977284A
; Patent No. 5558988
;  GENERAL INFORMATION:
;    APPLICANT:  Prockop, Darwin J.
;    APPLICANT:  Ala-Kokko, Leena
;    APPLICANT:  Williams, Charlene J.
;    APPLICANT:  Ritvaniemi, Pertti
;    APPLICANT:  Baldwin, Clinton
;    APPLICANT:  Hopkinson, Ian
;    APPLICANT:  Ahmad, Nilofer Nina
;    TITLE OF INVENTION:  METHODS OF DETECTING A GENETIC
;    TITLE OF INVENTION:  PREDISPOSITION FOR OSTEOARTHRITIS
;    NUMBER OF SEQUENCES:  261
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris
;      STREET:  One Liberty Place, 46th floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/977,284A
;       FILING DATE:  13-NOV-1992
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DeLuca, Mark
;       REGISTRATION NUMBER:  33,229
;       REFERENCE/DOCKET NUMBER:  TJU-0697
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 568-3100
;       TELEFAX:  (215) 568-3439
;   INFORMATION FOR SEQ ID NO:  248:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  67
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
;     ANTI-SENSE:  NO
US-07-977-284A-248

  Query Match             86.7%;  Score 13;  DB 1;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 CCGCCCGCTGAGG 15
           |||||||||||||
Db      33 CCGCCCGCTGAGG 45


RESULT 6
US-08-256-426B-248
; Sequence 248, Application US/08256426B
; Patent No. 5948611
;  GENERAL INFORMATION:
;     APPLICANT:  Prockop, Darwin J.
;     APPLICANT:  Ala-Kokko, Leena
;     APPLICANT:  Williams, Charlene J.
;     APPLICANT:  Ritvaniemi, Pertti
;     APPLICANT:  Baldwin, Clinton
;     APPLICANT:  Hopkinson, Ian
;     APPLICANT:  Ahmad, Nilofer Nina
;     TITLE OF INVENTION:  Methods of Detecting A Genetic
;     NUMBER OF SEQUENCES:  293
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
;       STREET:  One Liberty Place - 46th Floor
;       CITY:  Philadelphia
;       STATE:  PA
;       COUNTRY:  USA
;       ZIP:  19103
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  Windows 3.1
;       SOFTWARE:  WORDPERFECT 6.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/256,426B
;       FILING DATE:  03-FEB-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/10964
;       FILING DATE:  12-NOV-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/977,284
;       FILING DATE:  13-NOV-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Mark DeLuca
;       REGISTRATION NUMBER:  33,229
;       REFERENCE/DOCKET NUMBER:  TJU-1082
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 568-3100
;       TELEFAX:  (215) 568-3439
;   INFORMATION FOR SEQ ID NO:  248:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  67
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
;     ANTI-SENSE:  NO
US-08-256-426B-248

  Query Match             86.7%;  Score 13;  DB 2;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 CCGCCCGCTGAGG 15
           |||||||||||||
Db      33 CCGCCCGCTGAGG 45


RESULT 7
US-08-403-852D-7
; Sequence 7, Application US/08403852D
; Patent No. 5891695
;  GENERAL INFORMATION:
;     APPLICANT:  Blanc, Veronique
;     APPLICANT:  Blanche, Francis
;     APPLICANT:  Crouzet, Joel
;     APPLICANT:  Jacques, Nathalie
;     APPLICANT:  Lacroix, Patricia
;     APPLICANT:  Thibaut, Denis
;     APPLICANT:  Zagorec, Monique
;     APPLICANT:  Debussche, Laurent
;     APPLICANT:  De Crecy-Lagard, Valerie
;     TITLE OF INVENTION:  Polypeptides Involved In The
;     TITLE OF INVENTION:  Biosynthesis Of Streptogramins, Nucleotide Sequences
;     TITLE OF INVENTION:  Coding For These Polypeptides And Their Use
;     NUMBER OF SEQUENCES:  43
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett & Dunner
;       STREET:  1300 I Street, N.W., Suite 700
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20005-3315
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/403,852D
;       FILING DATE:  10-MAY-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/FR 93/00923
;       FILING DATE:  25-SEP-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  FR 92/11441
;       FILING DATE:  25-SEP-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Meyers, Kenneth J.
;       REGISTRATION NUMBER:  25,146
;       REFERENCE/DOCKET NUMBER:  03806.0054-00000
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 408-4000
;       TELEFAX:  (202) 408-4400
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  695 base pairs
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  S.pristinaespiralis
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  212..695
;      OTHER INFORMATION:  /product= "Gene SnaC"
US-08-403-852D-7

  Query Match             86.7%;  Score 13;  DB 2;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 CCGCCCGCTGAGG 15
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Db     170 CCGCCCGCTGAGG 182


RESULT 8
US-08-510-646B-7
; Sequence 7, Application US/08510646B
; Patent No. 6077699
;  GENERAL INFORMATION:
;    APPLICANT:  Blanc, Veronique
;    APPLICANT:  Blanche, Francis
;    APPLICANT:  Crouzet, Joel
;    APPLICANT:  Jacques, Nathalie
;    APPLICANT:  Lacroix, Patricia
;    APPLICANT:  Thibaut, Denis
;    APPLICANT:  Zagorec, Monique
;    APPLICANT:  Debussche, Laurent
;    APPLICANT:  De Crecy-Lagard, Valerie
;    TITLE OF INVENTION:  Polypeptides Involved In The
;    TITLE OF INVENTION:  Biosynthesis Of Streptogramins, Nucleotide Sequences
;    TITLE OF INVENTION:  Coding For These Polypeptides And Their Use
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett & Dunner
;      STREET:  1300 I Street, N.W., Suite 700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/510,646B
;      FILING DATE:  03-AUG-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/403,852
;      FILING DATE:  10-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/FR 93/00923
;      FILING DATE:  25-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 92/11441
;      FILING DATE:  25-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  03806.0054-01000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400

;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  695 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  S.pristinaespiralis
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  212..695
;      OTHER INFORMATION:  /product= "Gene SnaC"
US-08-510-646B-7

  Query Match             86.7%;  Score 13;  DB 3;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 CCGCCCGCTGAGG 15
           |||||||||||||
Db     170 CCGCCCGCTGAGG 182


RESULT 9
US-09-231-818-7
; Sequence 7, Application US/09231818
; Patent No. 6171846
;  GENERAL INFORMATION:
;    APPLICANT:  Blanc, Veronique
;    APPLICANT:  Blanche, Francis
;    APPLICANT:  Crouzet, Joel
;    APPLICANT:  Jacques, Nathalie
;    APPLICANT:  Lacroix, Patricia
;    APPLICANT:  Thibaut, Denis
;    APPLICANT:  Zagorec, Monique
;    APPLICANT:  Debussche, Laurent
;    APPLICANT:  De Crecy-Lagard, Valerie
;    TITLE OF INVENTION:  Polypeptides Involved In The
;    TITLE OF INVENTION:  Biosynthesis Of Streptogramins, Nucleotide Sequences
;    TITLE OF INVENTION:  Coding For These Polypeptides And Their Use
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett & Dunner
;      STREET:  1300 I Street, N.W., Suite 700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/231,818
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,852
;      FILING DATE:  10-MAY-1995
;      APPLICATION NUMBER:  PCT/FR 93/00923
;      FILING DATE:  25-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 92/11441
;      FILING DATE:  25-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  03806.0054-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
```

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;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  695 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  S.pristinaespiralis
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  212..695
;      OTHER INFORMATION:  /product= "Gene SnaC"
US-09-231-818-7

  Query Match             86.7%;  Score 13;  DB 4;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 CCGCCCGCTGAGG 15
           |||||||||||||
Db     170 CCGCCCGCTGAGG 182


RESULT 10
US-08-651-136C-25/c
; Sequence 25, Application US/08651136C
; Patent No. 6001639
;  GENERAL INFORMATION:
;    APPLICANT:  Schulein, Martin
;    APPLICANT:  Andersen, Lene N.
;    APPLICANT:  Lassen, Soren F.
;    APPLICANT:  Kauppinen, Markus S.
;    APPLICANT:  Lange, Lene
;    APPLICANT:  Nielsen, Ruby I.
;    APPLICANT:  Ihara, Michiko
;    APPLICANT:  Takagi, Shinobu
;    TITLE OF INVENTION:  No. 6001639el Endoglucanases
;    NUMBER OF SEQUENCES:  109
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6001639o No. 6001639disk of No. 6001639th America, Inc.
;      STREET:  405 Lexington Avenue, 64th Floor
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/651,136C
;      FILING DATE:  21-MAY-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4366.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-867-0123
;      TELEFAX:  212-878-9655
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  425 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  12..425
US-08-651-136C-25

  Query Match             82.7%;  Score 12.4;  DB 3;  Length 425;
  Best Local Similarity   92.9%;  Pred. No. 3.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAG 14
           |||| |||||||||
Db     319 GTCCCCCCGCTGAG 306


RESULT 11
US-08-478-507-12/c
; Sequence 12, Application US/08478507
; Patent No. 6120988
;  GENERAL INFORMATION:
;    APPLICANT:  Reyes, Gregory R
;    APPLICANT:  Yarbough, Patrice O
;    APPLICANT:  Bradley, Daniel W
;    APPLICANT:  Krawczynski, Krzysztof Z
;    APPLICANT:  Tam, Albert
;    APPLICANT:  Fry, Kirk E
;    TITLE OF INVENTION:  DNA Sequences of Enterically Transmitted
;    TITLE OF INVENTION:  No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,507
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/279,823
;      FILING DATE:  25-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/681,078
;      FILING DATE:  05-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/505,888
;      FILING DATE:  05-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/420,921
;      FILING DATE:  13-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/367,486
;      FILING DATE:  16-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/336,672
;      FILING DATE:  11-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/208,997
;      FILING DATE:  17-JUN-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sholtz, Charles K.
;      REGISTRATION NUMBER:  38,615
;      REFERENCE/DOCKET NUMBER:  4600-0183.22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 324-0880
;      TELEFAX:  (650) 324-0960
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  874 base pairs
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Tashkent strain
US-08-478-507-12

  Query Match             82.7%;  Score 12.4;  DB 3;  Length 874;
  Best Local Similarity   92.9%;  Pred. No. 3.8e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TCCGCCCGCTGAGG 15
           |||||||||| |||
Db     853 TCCGCCCGCTCAGG 840


RESULT 12
US-09-128-275A-12/c
; Sequence 12, Application US/09128275A
; Patent No. 6229005
;  GENERAL INFORMATION:
;    APPLICANT:  Reyes, Gregory R
;    APPLICANT:  Yarbough, Patrice O
;    APPLICANT:  Bradley, Daniel W
;    APPLICANT:  Krawczynski, Krzysztof Z
;    APPLICANT:  Tam, Albert
;    APPLICANT:  Fry, Kirk E
;    TITLE OF INVENTION:  DNA Sequences of Enterically Transmitted
;    TITLE OF INVENTION:  No. 6229005-A/No. 6229005-B Hepatitis Viral Agent
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/128,275A
;      FILING DATE:  03-AUG-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/279,823
;      FILING DATE:  25-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/681,078
;      FILING DATE:  05-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/505,888
;      FILING DATE:  05-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/420,921
;      FILING DATE:  13-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/367,486
;      FILING DATE:  16-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/336,672
;      FILING DATE:  11-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/208,997
;      FILING DATE:  17-JUN-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petithory, Joanne R.
;      REGISTRATION NUMBER:  42,995
;      REFERENCE/DOCKET NUMBER:  4600-0183.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 324-0880
;      TELEFAX:  (650) 324-0960
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  874 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Tashkent strain
US-09-128-275A-12

  Query Match             82.7%;  Score 12.4;  DB 4;  Length 874;
  Best Local Similarity   92.9%;  Pred. No. 3.8e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TCCGCCCGCTGAGG 15
           |||||||||| |||
Db     853 TCCGCCCGCTCAGG 840


RESULT 13
US-08-456-200B-17
; Sequence 17, Application US/08456200B
; Patent No. 6229000
;  GENERAL INFORMATION:
;    APPLICANT:  Franz, Jurgen; Weingartner, Bernhard;
;    APPLICANT:  Unterbeck, Axel; Rae, Peter
;    TITLE OF INVENTION:  TISSUE-SPECIFIC HUMAN NEURONAL
;    TITLE OF INVENTION:  CALCIUM CHANNEL SUB-TYPES AND
;    TITLE OF INVENTION:  THEIR USE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SPRUNG HORN KRAMER & WOODS
;      STREET:  660 White Plains Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10591-5144
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MB
;      MEDIUM TYPE:  storage
;      COMPUTER:  NEC Powermate SX/20
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/456,200B
;      FILING DATE:  31-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/094,712
;      FILING DATE:  19-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/858,278
;      FILING DATE:  26-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,778
;      FILING DATE:  19-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 41 10 785
;      FILING DATE:  04-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kurt G. Briscoe
;      REGISTRATION NUMBER:  33,141
;      REFERENCE/DOCKET NUMBER:  Bayer 8398.3-KGB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 332-1700
;      TELEFAX:  (914) 332-1844
;      TELEX:
```

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;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1100 nucleotides
;      TYPE:  Nucleotide
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA
US-08-456-200B-17

  Query Match             82.7%;  Score 12.4;  DB 4;  Length 1100;
  Best Local Similarity   92.9%;  Pred. No. 3.8e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TCCGCCCGCTGAGG 15
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Db     906 TCCGCCTGCTGAGG 919


RESULT 14
US-08-478-507-1/c
; Sequence 1, Application US/08478507
; Patent No. 6120988
;  GENERAL INFORMATION:
;    APPLICANT:  Reyes, Gregory R
;    APPLICANT:  Yarbough, Patrice O
;    APPLICANT:  Bradley, Daniel W
;    APPLICANT:  Krawczynski, Krzysztof Z
;    APPLICANT:  Tam, Albert
;    APPLICANT:  Fry, Kirk E
;    TITLE OF INVENTION:  DNA Sequences of Enterically Transmitted
;    TITLE OF INVENTION:  No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,507
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/279,823
;      FILING DATE:  25-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/681,078
;      FILING DATE:  05-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/505,888
;      FILING DATE:  05-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/420,921
;      FILING DATE:  13-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/367,486
;      FILING DATE:  16-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/336,672
;      FILING DATE:  11-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/208,997
;      FILING DATE:  17-JUN-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sholtz, Charles K.
;      REGISTRATION NUMBER:  38,615
;      REFERENCE/DOCKET NUMBER:  4600-0183.22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 324-0880
;      TELEFAX:  (650) 324-0960
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1295 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  1.33 kb EcoRI insert of ET1.1,
;      INDIVIDUAL ISOLATE:  forward sequence
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1293
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..1294
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..1295
US-08-478-507-1

  Query Match             82.7%;  Score 12.4;  DB 3;  Length 1295;
  Best Local Similarity   92.9%;  Pred. No. 3.7e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TCCGCCCGCTGAGG 15
           |||||||||| |||
Db    1112 TCCGCCCGCTCAGG 1099


RESULT 15
US-08-478-507-5
; Sequence 5, Application US/08478507
; Patent No. 6120988
;  GENERAL INFORMATION:
;    APPLICANT:  Reyes, Gregory R
;    APPLICANT:  Yarbough, Patrice O
;    APPLICANT:  Bradley, Daniel W
;    APPLICANT:  Krawczynski, Krzysztof Z
;    APPLICANT:  Tam, Albert
;    APPLICANT:  Fry, Kirk E
;    TITLE OF INVENTION:  DNA Sequences of Enterically Transmitted
;    TITLE OF INVENTION:  No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,507
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/279,823
;      FILING DATE:  25-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/681,078
;      FILING DATE:  05-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/505,888
;      FILING DATE:  05-APR-1990
;    PRIOR APPLICATION DATA:
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;       APPLICATION NUMBER:  US 07/420,921
;       FILING DATE:  13-OCT-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/367,486
;       FILING DATE:  16-JUN-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/336,672
;       FILING DATE:  11-APR-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/208,997
;       FILING DATE:  17-JUN-1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Sholtz, Charles K.
;       REGISTRATION NUMBER:  38,615
;       REFERENCE/DOCKET NUMBER:  4600-0183.22
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (650) 324-0880
;       TELEFAX:  (650) 324-0960
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1295 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       INDIVIDUAL ISOLATE:  1.33 kb EcoRI insert of ET1.1,
;       INDIVIDUAL ISOLATE:  reverse sequence
US-08-478-507-5

  Query Match             82.7%;  Score 12.4;  DB 3;  Length 1295;
  Best Local Similarity   92.9%;  Pred. No. 3.7e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TCCGCCCGCTGAGG 15
           ||||||||||  |||
Db     184 TCCGCCCGCTCAGG 197


Search completed: November  2, 2002, 16:50:51
Job time : 15.9091 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 16:08:01 ; Search time 539.591 Seconds
(without alignments)
375.200 Million cell updates/sec

Title: US-09-856-803-5
Perfect score: 15
Sequence: 1 gtccgcccgctgagg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	287	10	BI401298	BI401298 MI-P-CP0-
	2	15	100.0	288	10	BI399298	BI399298 MI-P-AY1-
	3	15	100.0	291	10	BI404045	BI404045 MI-P-CP1-
	4	15	100.0	295	10	BI401112	BI401112 MI-P-CP0-
	5	15	100.0	301	10	BI401773	BI401773 MI-P-CP0-
	6	15	100.0	302	10	BI402471	BI402471 MI-P-CP0-
c	7	15	100.0	310	10	BG733338	BG733338 347193 MA
c	8	15	100.0	328	9	BE235921	BE235921 143549 MA
c	9	15	100.0	336	10	BG895911	BG895911 359598 MA
	10	15	100.0	360	10	BI401388	BI401388 MI-P-CP0-
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	12	15	100.0	386	10	BI399086	BI399086 MI-P-AY1-
	13	15	100.0	393	10	BF709326	BF709326 MI-P-AY0-
c	14	15	100.0	406	10	BG733337	BG733337 347192 MA
	15	15	100.0	406	10	BE245562	BE245562 TCBAP1E21
	16	15	100.0	417	10	BF708610	BF708610 MI-P-AY0-
	17	15	100.0	424	10	BI401812	BI401812 MI-P-CP0-
	18	15	100.0	426	10	BF709186	BF709186 MI-P-AY0-
	19	15	100.0	490	12	CNS03GY5	AL243590 Tetraodon
c	20	15	100.0	504	10	BF191238	BF191238 238007 MA
	21	15	100.0	524	10	BI398712	BI398712 MI-P-AY1-
c	22	15	100.0	569	10	BI341125	BI341125 368445 MA
	23	15	100.0	646	10	BI911023	BI911023 603068746
c	24	14.6	97.3	1073	12	CNS03D33	AL238584 Tetraodon
c	25	14	93.3	54	12	AZ918075	AZ918075 1006003B0
c	26	14	93.3	244	9	AA368591	AA368591 EST79689
c	27	14	93.3	304	9	AA359696	AA359696 EST690?9
c	28	14	93.3	322	9	AA323834	AA323834 EST266?2
c	29	14	93.3	327	9	AA193211	AA193211 zp94h05.r
c	30	14	93.3	341	9	AW158718	AW158718 za45d08.x
	31	14	93.3	410	10	BG898450	BG898450 HOA9-1-D9
	32	14	93.3	411	10	BG896316	BG896316 HOA29-1-C
c	33	14	93.3	424	9	AW765719	AW765719 da76b03.y
c	34	14	93.3	444	10	BG160579	BG160579 df35f07.y
c	35	14	93.3	446	9	AV748509	AV748509 AV748509
c	36	14	93.3	449	10	BG364899	BG364899 dc93a11.y
c	37	14	93.3	461	9	AI824086	AI824086 wj46a04.x
c	38	14	93.3	471	10	W05270	W05270 za83c05.r1
c	39	14	93.3	482	9	AW766154	AW766154 da82h09.y
	40	14	93.3	489	10	BG899553	BG899553 HOA24-1-G
c	41	14	93.3	490	9	BE190122	BE190122 db65e05.y
c	42	14	93.3	491	10	BE680239	BE680239 df76g04.y
c	43	14	93.3	503	9	AW381237	AW381237 RC0-HT029
c	44	14	93.3	505	10	BM288253	BM288253 529229 MA
c	45	14	93.3	509	9	AI738677	AI738677 wi11h06.x

ALIGNMENTS

RESULT 1
BI401298
LOCUS BI401298 287 bp mRNA linear EST 14-AUG-2001
DEFINITION MI-P-CP0-nvm-d-02-0-UI.s1 MI-P-CP0 Sus scrofa cDNA clone MI-P-CP0-nvm-d-02-0-UI 3', mRNA sequence.
ACCESSION BI401298
VERSION BI401298.1 GI:15180359
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 287)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: cktuggle@iastate.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized uterus library cDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .287
/organism="Sus scrofa"
/db_xref="taxon:9823"

/clone="MI-P-CP0-nvm-d-02-0-UI"
/clone_lib="MI-P-CP0"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CP0 library is derived from uterus. For a detailed description of the library from which this clone was derived, please visit our web site at http://pigest.genome.iastate.edu/. The procedure used to create this library has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=MI-P-CP0
TAG_TISSUE=uterus
TAG_SEQ=AGTCCAATCG"
BASE COUNT 77 a 68 c 78 g 64 t
ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCCGCTGAGG 15
||||||||||||||||
Db 237 GTCCGCCCGCTGAGG 251

RESULT 2
BI399298
LOCUS BI399298 288 bp mRNA linear EST 14-AUG-2001
DEFINITION MI-P-AY1-nrp-g-06-0-UI.s1 MI-P-AY1 Sus scrofa cDNA clone MI-P-AY1-nrp-g-06-0-UI 3', mRNA sequence.
ACCESSION BI399298
VERSION BI399298.1 GI:15178359
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 288)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: cktuggle@iastate.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized placenta library cDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .288
/organism="Sus scrofa"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone="MI-P-AY1-nrp-g-06-0-UI"
/clone_lib="MI-P-AY1"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-AY1 library is normalized library derived from the MI-P-AY0 library, ultimately derived from placenta tissue. For a detailed description of the library from which this clone was derived, please visit our web site at http://pigest.genome.iastate.edu/. The procedure used to create this library has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)
TAG_LIB=MI-P-AY1
TAG_TISSUE=placenta
TAG_SEQ=ATTGG"
BASE COUNT 80 a 67 c 78 g 63 t
ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCCGCTGAGG 15
||||||||||||||||
Db 237 GTCCGCCCGCTGAGG 251

RESULT 3
BI404045
LOCUS BI404045 291 bp mRNA linear EST 14-AUG-2001
DEFINITION MI-P-CP1-nwv-f-11-0-UI.s1 MI-P-CP1 Sus scrofa cDNA clone MI-P-CP1-nwv-f-11-0-UI 3', mRNA sequence.
ACCESSION BI404045
VERSION BI404045.1 GI:15183234
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 291)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: cktuggle@iastate.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .291
/organism="Sus scrofa"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone="MI-P-CP1-nwv-f-11-0-UI"
/clone_lib="MI-P-CP1"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CP1 library is normalized library derived from the MI-P-CP0 library, ultimately derived from uterus tissue. For a detailed description of the library from which this clone was derived, please visit our web site at http://pigest.genome.iastate.edu/. The procedure used to create this library has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)
TAG_SEQ=None found"

```
:E COUNT        73 a     70 c     83 g     65 t
:GIN

Query Match             100.0%;  Score 15;  DB 10;  Length 291;
Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

      1 GTCCGCCCGCTGAGG 15
        |||||||||||||||
,   236 GTCCGCCCGCTGAGG 250


ESULT 4
1401112
OCUS        BI401112                295 bp    mRNA    linear   EST 14-AUG-2001
EFINITION   MI-P-CP0-nvi-c-03-0-UI.s1 MI-P-CP0 Sus scrofa cDNA clone
            MI-P-CP0-nvi-c-03-0-UI 3', mRNA sequence.

CCESSION    BI401112
ERSION      BI401112.1  GI:15180173
EYWORDS     EST.
OURCE       pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

EFERENCE    1  (bases 1 to 295)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
OMMENT      Contact: Tuggle CK
            Molecular Genetics Laboratory, Department of Animal Science
            Iowa State University
            201 Kildee Hall, Ames, IA 50011-3150, USA
            Tel: 5152944252
            Fax: 5152942401
            Email: cktuggle@iastate.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            non-normalized uterus library cDNA Library Preparation: M.B. Soares
            Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
            of Iowa Clone distribution: clones will be available through
            Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=Yes.
EATURES             Location/Qualifiers
     source         1. .295
                    /organism="Sus scrofa"
                    /db_xref="taxon:9823"
                    /clone="MI-P-CP0-nvi-c-03-0-UI"
                    /clone_lib="MI-P-CP0"
                    /lab_host="DH10B (Life Technologies)"
                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                    polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CP0
                    library is derived from uterus. For a detailed description
                    of the  library from which this clone was derived, please
                    visit our web site at  http://pigest.genome.iastate.edu/.
                    The procedure used to create this library has been
                    previously described (Bonaldo, Lennon and Soares, Genome
                    Research 6:791-806, 1996)
                    TAG_LIB=MI-P-CP0
                    TAG_TISSUE=uterus
                    TAG_SEQ=AGTCCAATCG"

ASE COUNT       73 a     71 c     89 g     62 t
RIGIN

  Query Match           100.0%;  Score 15;  DB 10;  Length 295;
  Best Local Similarity 100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db    233 GTCCGCCCGCTGAGG 247


RESULT 5
BI401773
LOCUS       BI401773                301 bp    mRNA    linear   EST 14-AUG-2001
DEFINITION  MI-P-CP0-nvr-c-09-0-UI.s1 MI-P-CP0 Sus scrofa cDNA clone
            MI-P-CP0-nvr-c-09-0-UI 3', mRNA sequence.

ACCESSION   BI401773
VERSION     BI401773.1  GI:15180834
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE   1  (bases 1 to 301)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Tuggle CK
            Molecular Genetics Laboratory, Department of Animal Science
            Iowa State University
            201 Kildee Hall, Ames, IA 50011-3150, USA
            Tel: 5152944252
            Fax: 5152942401
            Email: cktuggle@iastate.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            non-normalized uterus library cDNA Library Preparation: M.B. Soares
            Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
            of Iowa Clone distribution: clones will be available through
            Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES            Location/Qualifiers
     source         1. .301
                    /organism="Sus scrofa"
                    /db_xref="taxon:9823"
                    /clone="MI-P-CP0-nvr-c-09-0-UI"
                    /clone_lib="MI-P-CP0"
                    /lab_host="DH10B (Life Technologies)"
                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                    polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CP0
                    library is derived from uterus. For a detailed description
                    of the  library from which this clone was derived, please
                    visit our web site at  http://pigest.genome.iastate.edu/.
                    The procedure used to create this library has been
                    previously described (Bonaldo, Lennon and Soares, Genome
                    Research 6:791-806, 1996)
                    TAG_LIB=MI-P-CP0
                    TAG_TISSUE=uterus
                    TAG_SEQ=AGTCCAATCG"

BASE COUNT      72 a     72 c     91 g     66 t
ORIGIN

  Query Match           100.0%;  Score 15;  DB 10;  Length 301;
  Best Local Similarity 100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db    236 GTCCGCCCGCTGAGG 250


RESULT 6
BI402471
```

; BI402471 302 bp mRNA linear EST 14-AUG-2001
ITION MI-P-CP0-nvx-g-02-0-UI.s1 MI-P-CP0 Sus scrofa cDNA clone MI-P-CP0-nvx-g-02-0-UI 3', mRNA sequence.
SION BI402471
ON BI402471.1 GI:15181532
RDS EST.
E pig.
ANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
ENCE 1 (bases 1 to 302)
HORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
LE Normalization and subtraction: two approaches to facilitate gene discovery
RNAL Genome Res. 6 (9), 791-806 (1996)
LINE 97044477
NT Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: cktuggle@iastate.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized uterus library cDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
RES Location/Qualifiers
source 1. .302
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone="MI-P-CP0-nvx-g-02-0-UI"
/clone_lib="MI-P-CP0"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CP0 library is derived from uterus. For a detailed description of the library from which this clone was derived, please visit our web site at http://pigest.genome.iastate.edu/. The procedure used to create this library has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=MI-P-CP0
TAG_TISSUE=uterus
TAG_SEQ=AGTCCAATCG"
COUNT 77 a 72 c 89 g 64 t
N

ry Match 100.0%; Score 15; DB 10; Length 302;
t Local Similarity 100.0%; Pred. No. 1.6e+03;
ches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTCCGCCCGCTGAGG 15
||||||||||||||
236 GTCCGCCCGCTGAGG 250

T 7
3338/c
; BG733338 310 bp mRNA linear EST 11-MAY-2001
NITION 347193 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
SSION BG733338
ION BG733338.1 GI:14019622
ORDS EST.
E pig.
ANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 310)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 109 row: 0 column: 24
Seq primer: ATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .310
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
BASE COUNT 52 a 100 c 85 g 73 t
ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCCGCTGAGG 15
||||||||||||||
Db 93 GTCCGCCCGCTGAGG 79

RESULT 8
BE235921/c
LOCUS BE235921 328 bp mRNA linear EST 10-JUL-2000
DEFINITION 143549 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE235921
VERSION BE235921.1 GI:9020639
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 328)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRimers

```
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 82  row: N  column: 13
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .328
                      /organism="Sus scrofa"
                      /db_xref="taxon:9823"
                      /clone_lib="MARC 1PIG"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                      Library made from pooled tissue from day 11, 13, 15, 20,
                      and 30 embryos."
BASE COUNT       72 a    100 c     83 g     73 t
ORIGIN

  Query Match             100.0%;  Score 15;  DB 9;  Length 328;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db     91 GTCCGCCCGCTGAGG 77


RESULT 9
BG895911/c
LOCUS       BG895911                 336 bp    mRNA    linear   EST 05-JUN-2001
DEFINITION  359598 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BG895911
VERSION     BG895911.1  GI:14306152
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 336)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 124  row: H  column: 11
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .336
                      /organism="Sus scrofa"
                      /db_xref="taxon:9823"
                      /clone_lib="MARC 1PIG"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                      Library made from pooled tissue from day 11, 13, 15, 20,
                      and 30 embryos."
BASE COUNT      137 a     69 c     66 g     64 t
ORIGIN

  Query Match             100.0%;  Score 15;  DB 10;  Length 336;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db     26 GTCCGCCCGCTGAGG 12


RESULT 10
BI401388
LOCUS       BI401388                 360 bp    mRNA    linear   EST 14-AUG-2001
DEFINITION  MI-P-CP0-nvk-f-07-0-UI.s1 MI-P-CP0 Sus scrofa cDNA clone
            MI-P-CP0-nvk-f-07-0-UI 3', mRNA sequence.
ACCESSION   BI401388
VERSION     BI401388.1  GI:15180449
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 360)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Tuggle CK
            Molecular Genetics Laboratory, Department of Animal Science
            Iowa State University
            201 Kildee Hall, Ames, IA 50011-3150, USA
            Tel: 5152944252
            Fax: 5152942401
            Email: cktuggle@iastate.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            non-normalized uterus library cDNA Library Preparation: M.B. Soares
            Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
            of Iowa Clone distribution: clones will be available through
            Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .360
                      /organism="Sus scrofa"
                      /db_xref="taxon:9823"
                      /clone="MI-P-CP0-nvk-f-07-0-UI"
                      /clone_lib="MI-P-CP0"
                      /lab_host="DH10B (Life Technologies)"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CP0
                      library is derived from uterus. For a detailed description
                      of the  library from which this clone was derived, please
                      visit our web site at  http://pigest.genome.iastate.edu/.
                      The procedure used to create this library has been
                      previously described (Bonaldo, Lennon and Soares, Genome
                      Research 6:791-806, 1996)
                      TAG_LIB=MI-P-CP0
                      TAG_TISSUE=uterus
                      TAG_SEQ=AGTCCAATCG"
BASE COUNT       82 a     98 c    103 g     77 t
ORIGIN

  Query Match             100.0%;  Score 15;  DB 10;  Length 360;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db    241 GTCCGCCCGCTGAGG 255
```

```
RESULT 11
BG610493/c
LOCUS       BG610493                376 bp    mRNA    linear   EST 17-APR-2001
DEFINITION  326435 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BG610493
VERSION     BG610493.1  GI:13660472
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 101  row: D  column: 20
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .376
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 1PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
BASE COUNT      125 a     98 c     80 g     73 t
ORIGIN

  Query Match            100.0%;  Score 15;  DB 10;  Length 376;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db     86 GTCCGCCCGCTGAGG 72


RESULT 12
BI399086
LOCUS       BI399086                386 bp    mRNA    linear   EST 14-AUG-2001
DEFINITION  MI-P-AY1-nrk-b-07-0-UI.s1 MI-P-AY1 Sus scrofa cDNA clone
            MI-P-AY1-nrk-b-07-0-UI 3', mRNA sequence.
ACCESSION   BI399086
VERSION     BI399086.1  GI:15178147
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Tuggle CK
            Molecular Genetics Laboratory, Department of Animal Science
            Iowa State University
            201 Kildee Hall, Ames, IA 50011-3150, USA
            Tel: 5152944252
            Fax: 5152942401
            Email: cktuggle@iastate.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            normalized placenta library cDNA Library Preparation: M.B. Soares
            Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
            of Iowa Clone distribution: clones will be available through
            Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Sus scrofa"
                     /strain="crossbreed"
                     /db_xref="taxon:9823"
                     /clone="MI-P-AY1-nrk-b-07-0-UI"
                     /clone_lib="MI-P-AY1"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-AY1
                     library is normalized library derived from the MI-P-AY0
                     library,  ultimately derived from placenta tissue. For a
                     detailed description of the  library from which this clone
                     was derived, please visit our web site at
                     http://pigest.genome.iastate.edu/. The procedure used to
                     create this library has been previously described (Bonaldo
                     , Lennon and Soares, Genome Research 6: 791-806, 1996)
                     TAG_LIB=MI-P-AY1
                     TAG_TISSUE=placenta
                     TAG_SEQ=ATTGG"
BASE COUNT       85 a    112 c    105 g     82 t      2 others
ORIGIN

  Query Match            100.0%;  Score 15;  DB 10;  Length 386;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db    236 GTCCGCCCGCTGAGG 250


RESULT 13
BF709326
LOCUS       BF709326                393 bp    mRNA    linear   EST 02-JAN-2001
DEFINITION  MI-P-AY0-nah-c-09-0-UI.s1 MI-P-AY0 Sus scrofa cDNA clone
            MI-P-AY0-nah-c-09-0-UI 3', mRNA sequence.
ACCESSION   BF709326
VERSION     BF709326.1  GI:12008803
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 393)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Tuggle CK
            Molecular Genetics Laboratory, Department of Animal Science
            Iowa State University
            201 Kildee Hall, Ames, IA 50011-3150, USA
            Tel: 5152944252
            Fax: 5152942401
```

Email: cktuggle@iastate.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized placenta library cDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .393
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone="MI-P-AY0-nah-c-09-0-UI"
/clone_lib="MI-P-AY0"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-AY0 library is derived from placenta. For a detailed description of the library from which this clone was derived, please visit our web site at http://pigest.genome.iastate.edu/. The procedure used to create this library has been previously described (Bonaldo , Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=MI-P-AY0
TAG_TISSUE=placenta
TAG_SEQ=ATTGG"

BASE COUNT 86 a 117 c 105 g 83 t 2 others
ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db    236 GTCCGCCCGCTGAGG 250
```

RESULT 14
BG733337/c
LOCUS BG733337 406 bp mRNA linear EST 11-MAY-2001
DEFINITION 347192 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BG733337
VERSION BG733337.1 GI:14019621
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 406)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 109 row: O column: 23
Seq primer: ATTTAGGTGACACTATAG.

FEATURES Location/Qualifiers
source 1. .406
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."

BASE COUNT 89 a 116 c 108 g 93 t
ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db     93 GTCCGCCCGCTGAGG 79
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RESULT 15
BE245562
LOCUS BE245562 406 bp mRNA linear EST 03-OCT-2001
DEFINITION TCBAP1E2132 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2132, mRNA sequence.
ACCESSION BE245562
VERSION BE245562.1 GI:9097308
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 406)
AUTHORS Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
TITLE Pediatric Leukemia cDNA Sequencing Project
JOURNAL Unpublished (2000)
COMMENT Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@txccc.org
Citation: Carninci,P. and Hayashizaki,Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer.

FEATURES Location/Qualifiers
source 1. .406
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCBAP2132"
/clone_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCCGCAGGAGGAG(T)VN 3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand was primed with a BamH1-dC primer [5'AGAGAGCTCGGATCCGCGGCCGCAATAATAATAAT(C) 3']. Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN

of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"

BASE COUNT 73 a 140 c 130 g 61 t 2 others
ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db     169 GTCCGCCCGCTGAGG 183
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Search completed: November 2, 2002, 17:57:05
Job time : 543.591 secs

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ACCESSION   BC012481
VERSION     BC012481.1  GI:15214693
KEYWORDS    MGC.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2063)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-AUG-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: villalon@bcm.tmc.edu.
            Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
            A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
            Muzny,D.M., Gibbs,R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 28 Row: k Column: 6
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 178203.
FEATURES             Location/Qualifiers
     source          1. .2063
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="MGC:21367 IMAGE:4538187"
                     /tissue_type="Prostate, adenocarcinoma."
                     /clone_lib="NIH_MGC_91"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             222. .1463
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                     /product="Similar to adrenergic, beta-2-, receptor,
                     surface"
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                     LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
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                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                     IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                     AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                     TVPSDNIDSPGRNCSTNDSLL"
BASE COUNT      512 a    522 c    498 g    531 t
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 9;  Length 2063;
  Best Local Similarity  95.0%;  Pred. No. 6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||||||||||||||| |
Db    157 CCCCGCCGTGGGTCCGCCTG 176


RESULT 12
HSBAR
LOCUS       HSBAR                   2305 bp    DNA     linear   PRI 12-SEP-1993
DEFINITION  Human gene for beta-adrenergic receptor (beta-2 subtype).
```

```
ACCESSION   Y00106
VERSION     Y00106.1  GI:29370
KEYWORDS    beta-adrenergic receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2305)
  AUTHORS   Schofield,P.R., Rhee,L.M. and Peralta,E.G.
  TITLE     Primary structure of the human beta-adrenergic receptor gene
  JOURNAL   Nucleic Acids Res. 15 (8), 3636 (1987)
  MEDLINE   87203400
REFERENCE   2  (bases 1 to 2305)
  AUTHORS   Schofield,P.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-OCT-1987)
FEATURES             Location/Qualifiers
     source          1. .2305
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                     /db_xref="taxon:9606"
                     /clone="lambdahbetaAR17"
                     /clone_lib="Maniatis human"
     CDS             794. .2035
                     /note="beta-adrenergic receptor (AA 1 - 413)"
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                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                     IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                     AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                     TVPSDNIDSQGRNCSTNDSLL"
     misc_feature    809. .817
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     misc_feature    836. .844
                     /note="N-linked glycosylation site"
     misc_feature    896. .967
                     /note="membrane spanning domain I"
     misc_feature    1007. .1078
                     /note="membrane spanning domain II"
     misc_feature    1114. .1180
                     /note="membrane spanning domain III"
     misc_feature    1247. .1315
                     /note="membrane spanning domain IV"
     misc_feature    1385. .1450
                     /note="membrane spanning domain V"
     misc_feature    1616. .1687
                     /note="membrane spanning domain VI"
     misc_feature    1712. .1774
                     /note="membrane spanning domain VII"
BASE COUNT      495 a    616 c    649 g    545 t
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 9;  Length 2305;
  Best Local Similarity  95.0%;  Pred. No. 5.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||||||||||||||| ||
Db    729 CCCCGCCGTGGGTCCGCCTG 748


RESULT 13
AX022517
LOCUS       AX022517                3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9937761.
ACCESSION   AX022517
VERSION     AX022517.1  GI:10046115
KEYWORDS    .
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 13:09:44 ; Search time 62.0455 Seconds
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Title: US-09-856-803-6
Perfect score: 15
Sequence: 1 gtccgcctgctgagg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15	100.0	15	21	AAA38787	Human beta2 adrene
2	15	100.0	2300	20	AAX61116	Human beta2-adrene
3	15	100.0	2305	21	AAA38340	Human beta-adrener
4	15	100.0	3451	20	AAZ00774	Human beta 2-adren
5	15	100.0	3451	20	AAZ00775	Human beta 2-adren
6	15	100.0	3451	20	AAZ00777	Human beta 2-adren
7	15	100.0	3451	20	AAZ00778	Human beta 2-adren
8	15	100.0	3451	20	AAZ00780	Human beta 2-adren
9	14	93.3	1100	13	AAQ29275	Human calcium chan
10	14	93.3	6131	22	AAS42187	Genomic sequence #
11	14	93.3	6131	22	AAK69784	Human immune/haema
12	14	93.3	6232	13	AAQ29269	Human calcium chan
13	14	93.3	7175	14	AAQ37818	Sequence encoding
14	14	93.3	7175	16	AAQ84658	Human neuronal cal
15	14	93.3	7175	19	AAV42686	DNA encoding human
16	14	93.3	7175	21	AAA71704	Human calcium chan
17	14	93.3	7266	19	AAV29059	Human calcium chan
18	14	93.3	7362	14	AAQ37817	Sequence encoding
19	14	93.3	7362	16	AAQ84657	Human neuronal cal
20	14	93.3	7362	19	AAV42685	DNA encoding human
21	14	93.3	7362	21	AAA71703	Human calcium chan
22	14	93.3	7376	20	AAX88001	N-type calcium cha
23	14	93.3	12222	22	AAF54045	Human alpha-1-anti
24	14	93.3	39651	23	ABL18856	Drosophila melanog
25	13.4	89.3	15	21	AAA38786	Human beta2 adrene
26	13.4	89.3	20	19	AAV30491	Canine beta-2 adre
27	13.4	89.3	36	16	AAT55545	Human relA hammerh
28	13.4	89.3	36	16	AAT55356	Human relA hammerh
29	13.4	89.3	36	16	AAT53180	Mouse ICAM hammerh
30	13.4	89.3	36	16	AAT53133	Mouse ICAM hammerh
31	13.4	89.3	36	16	AAT55178	*Mouse relA hammerh*
32	13.4	89.3	36	22	AAA95743	PKCalpha primer-pa
c 33	13.4	89.3	51	22	AAL31694	Human SNP oligonuc
34	13.4	89.3	51	22	AAH79739	Human DNA containi
c 35	13.4	89.3	59	20	AAZ25379	Human FLINT PCR pr
c 36	13.4	89.3	59	21	AAA51079	Forward primer for
37	13.4	89.3	230	22	AAH27139	Human beta-2 adren
c 38	13.4	89.3	308	18	AAT47503	Partial Enterobact
c 39	13.4	89.3	454	22	AAK93017	Human cDNA 3'-end
c 40	13.4	89.3	472	22	ABA52145	Human foetal liver
c 41	13.4	89.3	472	22	ABA21953	Probe #419 for gen
c 42	13.4	89.3	472	22	AAK00425	*Human brain expres*
c 43	13.4	89.3	472	22	AAK25868	Human bone marrow
c 44	13.4	89.3	472	22	AAI10498	Probe #431 for gen
c 45	13.4	89.3	472	22	AAI31752	Probe #438 used to

ALIGNMENTS

RESULT 1
AAA38787
ID AAA38787 standard; DNA; 15 BP.
XX
AC AAA38787;
XX
DT 05-OCT-2000 (first entry)
XX
DE Human beta2 adrenergic receptor beta2AR T allele-specific probe.
XX
KW Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW congestive heart failure; ischemic heart disease; arrhythmia;
KW obesity; diabetes; vascular disease; premature labour; migraine;
KW anaphylaxis; chronic obstructive pulmonary disease;
KW allele-specific oligonucleotide probe; ss.
XX
OS Homo sapiens.
XX
PN WO200031307-A1.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US27963.
XX
PR 25-NOV-1998; 98US-0109886.
XX
PA (UYCI-) UNIV CINCINNATI.
XX
PI Liggett SB;
XX
DR WPI; 2000-400107/34.

XX
PT Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT receptor (beta 2 AR), useful for predicting genetic disposition to a
PT disease modified by beta 2 AR expression e.g. congestive heart failure,
PT hypertension -
XX
PS Claim 5; Page 11; 56pp; English.
XX
CC The present sequence is an allele-specific oligonucleotide probe
CC for the T allele of the human beta2 adrenergic receptor (beta2AR) gene,
CC which is located on chromosome 5q31 (12). The gene has two different
CC alleles, and it has been shown that the presence of two copies of the T
CC allele leads to higher expression of the gene. This is because the
CC polymorphism is found in the 5' leader sequence, which encodes a peptide
CC which regulates expression of the beta2AR gene. The polymorphism is
CC thought to affect individuals' responses to beta-agonists and
CC beta-antagonists, and is likely to influence their predisposition to
CC asthma, hypertension, congestive heart failure, ischemic heart disease,
CC arrhythmia, obesity, diabetes, vascular disease, premature labour,
CC migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD).
CC The gene can, therefore, be used to predict the susceptibility of an
CC individual to these diseases and determine the best treatment.
XX
SQ Sequence 15 BP; 1 A; 5 C; 6 G; 3 T; 0 other;

Query Match 100.0%; Score 15; DB 21; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCTGCTGAGG 15
||||||||||||||||
Db 1 GTCCGCCTGCTGAGG 15

RESULT 2
AAX61116
ID AAX61116 standard; DNA; 2300 BP.
XX
AC AAX61116;
XX
DT 27-JUL-1999 (first entry)
XX
DE Human beta2-adrenergic receptor gene.
XX
KW Alpha1B-adrenergic receptor; human; cardiovascular disease;
KW beta2 adrenergic receptor; genetic variation identification; hypertrophy;
KW disease diagnosis; hypertension; prostatic disease; pulmonary disorder;
KW asthma; peripheral vascular disorder; neuropsychic disorder;
KW endocrine-metabolic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO9924454-A1.
XX
PD 20-MAY-1999.
XX
PF 04-NOV-1998; 98WO-US23496.
XX
PR 10-NOV-1997; 97US-0086232.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Buescher R, Herrmann V, Insel PA;
XX
DR WPI; 1999-327357/27.
XX
PT Pairs of oligonucleotides for amplifying adrenergic receptor genes
XX
PS Disclosure; Fig 2; 58pp; English.
XX
CC This sequence represents the human beta2-adrenergic receptor gene, and
CC is amplified by the primers of the invention. The primers are non-self
CC hybridising; contain at least 15 nucleotides (nt) and has a melting
CC temperature 50-85 deg. C. Each pair of primers is: non-cross-hybridising;
CC anneals to two distinct segments (separated by at least 400 nt); and
CC generates a homogeneous population of gene segments in a polymerase chain
CC reaction (PCR). At least one primer in the pair can extend a 3'-end
CC sequence complementary to a template sequence in a DNA polymerase
CC reaction. The primers are used to amplify segments of the alpha1B and
CC beta2 adrenergic receptor genes, particularly to identify genetic
CC variations for diagnosis of disease. Specifically variations in the
CC alpha1B gene are associated with cardiovascular disease, hypertension and
CC prostatic disease (hypertrophy), and those in the beta2 gene with
CC cardiovascular disease, hypertension and asthma, but variations may also
CC be associated with peripheral vascular, pulmonary, neuropsychic and
CC endocrine-metabolic disorders. These primers allow rapid and specific
CC amplification of large and homogeneous gene segments of the alpha1B and
CC beta2 genes from a complex mixture of DNAs. This makes possible detection
CC of genetic alterations not previously amenable to routine, automated and
CC large-scale sequencing analysis.
XX
SQ Sequence 2300 BP; 495 A; 613 C; 646 G; 546 T; 0 other;

Query Match 100.0%; Score 15; DB 20; Length 2300;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCTGCTGAGG 15
||||||||||||||||
Db 740 GTCCGCCTGCTGAGG 754

RESULT 3
AAA38340
ID AAA38340 standard; DNA; 2305 BP.
XX
AC AAA38340;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human beta-adrenergic receptor-2 coding region.
XX
KW Beta-adrenergic receptor-2 gene; coding region;
KW polymorphism; polymorphic marker; cardiovascular disease;
KW myocardial infarction; unstable angina; hypertension; atherosclerosis;
KW stroke; prognosis; drug screening; treatment outcome; human; ds.
XX
OS Homo sapiens.
XX
PN WO200022166-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-IB01678.
XX
PR 14-OCT-1998; 98US-0104286.
PR 14-OCT-1998; 98US-0104302.
XX
PA (EURO-) EURONA MEDICAL AB.
XX
PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
XX
DR WPI; 2000-318010/27.
XX
PT Assessing cardiovascular status in humans involves comparing test
PT polymorphic pattern comprising polymorphic positions within genes
PT encoding specific proteins, with reference polymorphic pattern -
XX
PS Disclosure; Page 124-125; 126pp; English.
XX
CC The invention relates to a novel method of assessing the cardiovascular
CC status in an individual and to newly identified polymorphisms in the
CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II
CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
CC aldosterone synthase, endothelin receptor type A and beta-adrenergic
CC receptors 1 and 2. The method comprises determining the sequence at one

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CC   or more polymorphic positions within these genes, and comparing the
CC   pattern of polymorphisms from the individual with a reference polymorphic
CC   pattern obtained from a population of individuals exhibiting a
CC   predetermined cardiovascular disease status. The polymorphic markers are
CC   useful for determining the predisposition of an individual to
CC   cardiovascular disorders such as myocardial infarction, unstable angina,
CC   hypertension, atherosclerosis and stroke. They are also useful for
CC   predicting the likely cardiovascular status of a patient given a
CC   treatment regimen comprising administration of cardiovascular drugs
CC   (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
CC   blockers) or calcium channel blockers). One or more polymorphic markers
CC   provides a basis for predicting the outcome of a treatment regimen.
CC   Fragments of the genes comprising a polymorphic site may be used as
CC   primers and probes for detecting genetic polymorphisms or in molecular
CC   library arrays for high throughput screening. The genes, and the proteins
CC   they encode are useful in the screening of potential cardiovascular
CC   drugs. Determination of an individual's polymorphic pattern reduces or
CC   eliminates trial and error in selecting a treatment for a particular
CC   individual cardiovascular patient. It also provides the ability to
CC   eliminate patients from clinical trials who are predicted to be
CC   non-responsive, or at a risk for an adverse response, to a particular
CC   treatment regimen. Adverse results in an early trial can be evaluated to
CC   identify polymorphic patterns so that the adverse results can be
CC   correlated with a sub-population of the test population, permitting
CC   exclusion of such sub-populations from the treatment group. Beneficial
CC   drugs can be approved for use in the appropriate population, thereby
CC   decreasing the number of patients required for a clinical trial, which in
CC   turn decreases the duration and cost of such trials. The present
CC   sequence represents the human beta-adrenergic receptor-2 gene
CC   coding region (GenBank Y00106/g293708). The polymorphic sites identified
CC   are 839A/G, 872C/G, 1045A/G, 1284C/T, 1316A/C, 1846C/G, 2032A/G,
CC   2068 no insert/G/C and 2070 no insert/C.
XX
SQ   Sequence 2305 BP; 495 A; 616 C; 649 G; 545 T; 0 other;

  Query Match             100.0%;  Score 15;  DB 21;  Length 2305;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCTGCTGAGG 15
           |||||||||||||||
Db     740 GTCCGCCTGCTGAGG 754


RESULT 4
AAZ00774
ID   AAZ00774 standard; DNA; 3451 BP.
XX
AC   AAZ00774;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 1.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(159,t)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(245,a)
FT                   /*tag=  b
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(565,g)
FT                   /*tag=  c
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(934,g)
FT                   /*tag=  d
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1120,g)
FT                   /*tag=  e
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1221,c)
FT                   /*tag=  f
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1541,t)
FT                   /*tag=  g
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773
FT                         and results in a change in the corresponding
FT                         wild type amino acid sequence from an Cys
FT                         residue to Arg residue"
FT   mutation        replace(1568,t)
FT                   /*tag=  h
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1633,a)
FT                   /*tag=  i
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773
FT                         and results in a change in the corresponding
FT                         wild type amino acid sequence from an Gly
FT                         residue to Arg residue"
FT   mutation        replace(1666,c)
FT                   /*tag=  j
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773
FT                         and results in a change in the corresponding
FT                         wild type amino acid sequence from an Glu
FT                         residue to Gln residue"
FT   mutation        replace(1839,g)
FT                   /*tag=  k
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(2078,c)
FT                   /*tag=  l
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773
FT                         and results in a change in the corresponding
FT                         wild type amino acid sequence from an Ile
FT                         residue to Thr residue"
FT   mutation        replace(2110,c)
FT                   /*tag=  m
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(2640,g)
FT                   /*tag=  n
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(2826,g)
FT                   /*tag=  o
FT                   /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
```

PR 30-DEC-1997; 97DE-1058401.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Hoehe M, Koepke K, Timmermann B;
XX
DR WPI; 1999-479048/40.
XX
PT Human beta2-adrenergic receptor gene variants, useful for
PT determining an individuals haplotype
XX
PS Claim 2; Fig 2a; 27pp; German.
XX
CC This invention describes novel variant human beta 2-adrenergic receptor
CC gene sequences which have hypotensive, cardiant, neuroprotective and
CC immunosuppressive activity. The products of the invention are used in a
CC method to determine a predisposition for high blood pressure as well as
CC for abnormal blood pressure and other cardiovascular diseases, including
CC myocardial infarction and stroke. Other conditions that can be
CC determined include neuropsychiatric disease, such as depression, anxiety,
CC attention deficit disorder with hyperactivity, eating disorders, e.g.
CC anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC and Riley-Day syndromes having selective noradrenergic-receptor
CC disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC disorders, and metabolic illnesses, e.g. morbid obesity including
CC predicting a change in weight, using body mass index, can also be
CC determined. The beta 2-adrenergic receptor sequence variants can be used
CC to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC 2-receptor agonists can be developed. Treatments can be optimized for
CC individuals, including gene therapy and pharmaceutical intervention
CC therapy. This sequence represents a variant of the wild type human beta
CC 2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ Sequence 3451 BP; 794 A; 871 C; 892 G; 894 T; 0 other;

Query Match 100.0%; Score 15; DB 20; Length 3451;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCTGCTGAGG 15
||||||||||||||||
Db 1534 GTCCGCCTGCTGAGG 1548

RESULT 5
AAZ00775
ID AAZ00775 standard; DNA; 3451 BP.
XX
AC AAZ00775;
XX
DT 07-OCT-1999 (first entry)
XX
DE Human beta 2-adrenergic receptor DNA variant 2.
XX
KW Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW cardiovascular disease; myocardial infarction; anxiety; depression;
KW neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW post-traumatic stress disorder; autonomous nervous system disease;
KW metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation replace(1541,c)
FT /*tag= a
FT /note= "This nucleotide differs from the wild type
FT nucleic acid sequence represented in AAZ00773
FT and results in a change in the corresponding
FT wild type amino acid sequence from an Cys
FT residue to Arg residue"
XX
PN WO9937761-A1.
XX
PD 29-JUL-1999.
XX
PF 30-DEC-1998; 98WO-DE03818.
XX
PR 30-DEC-1997; 97DE-1058401.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Hoehe M, Koepke K, Timmermann B;
XX
DR WPI; 1999-479048/40.
XX
PT Human beta2-adrenergic receptor gene variants, useful for
PT determining an individuals haplotype
XX
PS Claim 3; Fig 2a; 27pp; German.
XX
CC This invention describes novel variant human beta 2-adrenergic receptor
CC gene sequences which have hypotensive, cardiant, neuroprotective and
CC immunosuppressive activity. The products of the invention are used in a
CC method to determine a predisposition for high blood pressure as well as
CC for abnormal blood pressure and other cardiovascular diseases, including
CC myocardial infarction and stroke. Other conditions that can be
CC determined include neuropsychiatric disease, such as depression, anxiety,
CC attention deficit disorder with hyperactivity, eating disorders, e.g.
CC anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC and Riley-Day syndromes having selective noradrenergic-receptor
CC disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC disorders, and metabolic illnesses, e.g. morbid obesity including
CC predicting a change in weight, using body mass index, can also be
CC determined. The beta 2-adrenergic receptor sequence variants can be used
CC to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC 2-receptor agonists can be developed. Treatments can be optimized for
CC individuals, including gene therapy and pharmaceutical intervention
CC therapy. This sequence represents a variant of the wild type human beta
CC 2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ Sequence 3451 BP; 790 A; 872 C; 895 G; 894 T; 0 other;

Query Match 100.0%; Score 15; DB 20; Length 3451;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCTGCTGAGG 15
||||||||||||||||
Db 1534 GTCCGCCTGCTGAGG 1548

RESULT 6
AAZ00777
ID AAZ00777 standard; DNA; 3451 BP.
XX
AC AAZ00777;
XX
DT 07-OCT-1999 (first entry)
XX
DE Human beta 2-adrenergic receptor DNA variant 4.
XX
KW Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW cardiovascular disease; myocardial infarction; anxiety; depression;
KW neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW post-traumatic stress disorder; autonomous nervous system disease;
KW metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW ss.
XX

```
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1541,c)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
FT   mutation        replace(1633,a)
FT                   /*tag=  b
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 5; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 789 A; 872 C; 896 G; 894 T; 0 other;

  Query Match            100.0%;  Score 15;  DB 20;  Length 3451;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCTGCTGAGG 15
          |||||||||||||||
Db   1534 GTCCGCCTGCTGAGG 1548


RESULT 7
AAZ00778
ID   AAZ00778 standard; DNA; 3451 BP.
XX
AC   AAZ00778;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 5.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1541,c)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 6; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 790 A; 872 C; 895 G; 894 T; 0 other;

  Query Match            100.0%;  Score 15;  DB 20;  Length 3451;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 GTCCGCCTGCTGAGG 15
          ||||||||||||||||
Db   1534 GTCCGCCTGCTGAGG 1548


RESULT 8
AAZ00780
ID   AAZ00780 standard; DNA; 3451 BP.
XX
AC   AAZ00780;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 7.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1541,t)
FT                   /*tag= g
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
FT   mutation        replace(1633,a)
FT                   /*tag= b
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 8; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 789 A; 872 C; 896 G; 894 T; 0 other;

  Query Match             100.0%;  Score 15;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCTGCTGAGG 15
          ||||||||||||||||
Db   1534 GTCCGCCTGCTGAGG 1548


RESULT 9
AAQ29275
ID   AAQ29275 standard; DNA; 1100 BP.
XX
AC   AAQ29275;
XX
DT   03-MAR-1993  (first entry)
XX
DE   Human calcium channel 27980/17.
XX
KW   Plasmid pRR14-35; Ca-flux assay; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1012
FT                   /*tag= a
FT                   /note= "undefined"
FT   misc_difference 1037..1039
FT                   /*tag= b
FT                   /note= "undefined"
FT   misc_difference 1051
FT                   /*tag= c
FT                   /note= "undefined"
FT   misc_difference 1061
FT                   /*tag= d
FT                   /note= "undefined"
FT   misc_difference 1062
FT                   /*tag= e
FT                   /note= "undefined"
XX
PN   EP507170-A.
XX
PD   07-OCT-1992.
XX
PF   23-MAR-1992;   92EP-0104970.
XX
PR   04-APR-1991;   91DE-4110785.
XX
PA   (FARB ) BAYER AG.
XX
PI   Franz J,  Rae P,  Unterbeck A,  Weingaertner B;
XX
DR   WPI; 1992-333446/41.
DR   P-PSDB; AAR27655.
XX
PT   Cloned human neuronal calcium channel sub-types - useful in
PT   calcium flux assays to screen for neurone-specific calcium
PT   channel ligands
XX
PS   Claim 2; Page 96-98; 101pp; German.
```

XX
CC Human neuroblastoma cell line, hippocampus, frontal and temporal
CC cortex and visual cortex cDNA banks were screened with a probe
CC containing carp skeletal muscle Ca-channel cDNA. The cDNA clone
CC pRR14-35 is 3400bp long; the 5' 1100bp were sequenced and found to
CC overlap the clone pR14-5.3.3.1 (see AAQ29269). The sequence
CC can be inserted into a eukaryotic expression vector for use in
CC transforming suitable host cells. Cell lines producing human neuronal
CC calcium channel proteins can be used for screening for Ca channel
CC ligands (agonists or antagonists). See also AAQ29259-Q29274.
XX
SQ Sequence 1100 BP; 219 A; 295 C; 327 G; 252 T; 7 other;

Query Match 93.3%; Score 14; DB 13; Length 1100;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCCGCCTGCTGAGG 15
||||||||||||||
Db 906 TCCGCCTGCTGAGG 919

RESULT 10
AAS42187
ID AAS42187 standard; DNA; 6131 BP.
XX
AC AAS42187;
XX
DT 17-DEC-2001 (first entry)
XX
DE *Genomic sequence* #503 encoding novel human enzyme polypeptide.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotropic; anticoagulant; ds.
XX
OS Homo sapiens.
XX
PN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01239.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
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PR 16-MAR-2000; 2000US-0189874.
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PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
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PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465566/50.
XX
PT Novel polypeptides and polynucleotides useful for diagnosing,
PT preventing, treating neural, immune system, muscular, reproductive,
PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous
PT diseases -
XX
PS Disclosure; SEQ ID No 2313; 1180pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders
CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
CC blood-related disorders (e.g. haemophilia), reproductive disorders
CC (e.g. infertility) and infectious disorders (e.g. Influenza). The
CC polynucleotides of the invention can also be used in gene therapy.
CC AAS41685-AAS42192 represent DNA sequences encoding for the novel human
CC enzyme polypeptides of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 6131 BP; 1422 A; 1665 C; 1561 G; 1483 T; 0 other;

Query Match 93.3%; Score 14; DB 22; Length 6131;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCTGCTGAG 14
||||||||||||||
Db 379 GTCCGCCTGCTGAG 392

RESULT 11
AAK69784
ID AAK69784 standard; DNA; 6131 BP.
XX
AC AAK69784;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24596.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
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PR 01-NOV-2000; 2000US-0244617.
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PR 01-DEC-2000; 2000US-0250160.
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PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 24596; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 6131 BP; 1422 A; 1665 C; 1561 G; 1483 T; 0 other;

Query Match 93.3%; Score 14; DB 22; Length 6131;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCTGCTGAG 14
||||||||||||||
Db 379 GTCCGCCTGCTGAG 392

RESULT 12
AAQ29269
ID AAQ29269 standard; DNA; 6232 BP.
XX
AC AAQ29269;
XX
DT 03-MAR-1993 (first entry)
XX
DE Human calcium channel 27980/11.
XX
KW Plasmid pR14-5.3.3.1; Ca-flux assay; ss.

```
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   polyA_signal    6215..6220
FT                   /*tag= a
FT   repeat_unit     1..252
FT                   /*tag= b
FT                   /standard_name= Alu_repeat
FT                   /note= "possible cloning artefact"
FT   CDS             253..6048
FT                   /*tag= c
FT                   /note= "amino acids 358 to C-terminus
FT                        i.e. Domains II to IV"
FT   misc_difference 3746
FT                   /*tag= d
FT                   /note= "undefined"
XX
PN   EP507170-A.
XX
PD   07-OCT-1992.
XX
PF   23-MAR-1992;   92EP-0104970.
XX
PR   04-APR-1991;   91DE-4110785.
XX
PA   (FARB ) BAYER AG.
XX
PI   Franz J,  Rae P,  Unterbeck A,  Weingaertner B;
XX
DR   WPI; 1992-333446/41.
DR   P-PSDB; AAR27649.
XX
PT   Cloned human neuronal calcium channel sub-types - useful in
PT   calcium flux assays to screen for neurone-specific calcium
PT   channel ligands
XX
PS   Claim 2; Page 63-77; 101pp; German.
XX
CC   Human neuroblastoma cell line, hippocampus, frontal and temporal
CC   cortex and visual cortex cDNA banks were screened with a probe
CC   containing carp skeletal muscle Ca-channel cDNA. The cDNA clone
CC   pR14-5.3.3.1 overlaps with clone p1247-14.1.1.1 (see AAQ29263). The
CC   following differences are observed between the two sequences
CC   (nucleotide and position in pR14-5.3.3.1 given in brackets):
CC   1.Cytosine at position 520 (T: 3507); no change in deduced amino
CC   acid sequence. 2.Cytosine at position 775 (G; 3768); no change in
CC   deduced AA sequence. 3.Cytosine at position 1617 (T;4611).
CC   4.Adenosine at position 2360 (G; 5353). 5.deletion of 6 nucleotides
CC   at position 708 (CGGAAA; 3695-3700). 6. deletion of an Adenosine
CC   residue at position 1013 which leads to a stop codon at position
CC   1028-1030. 7. at position 3240 there are a further 2199 nucleotides
CC   of the 3'UTR which are absent from pR14-5.3.3.1. (The deletion of
CC   Adenosine at position 1013 is thought to be a cloning artefact).
CC   The sequence can be inserted into a eukaryotic expression vector for
CC   use in transforming suitable host cells. Cell lines producing human
CC   neuronal calcium channel proteins can be used for screening for Ca
CC   channel ligands (agonists or antagonists). See also AAQ29259-Q29275.
XX
SQ   Sequence 6232 BP; 1250 A; 1914 C; 1827 G; 1240 T; 1 other;

  Query Match             93.3%;  Score 14;  DB 13;  Length 6232;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCTGCTGAGG 15
           ||||||||||||||
Db     770 TCCGCCTGCTGAGG 783


RESULT 13
AAQ37818
ID   AAQ37818 standard; cDNA; 7175 BP.
XX
AC   AAQ37818;
XX
DT   30-JUN-1993  (first entry)
XX
DE   Sequence encoding the alpha 1B-2 human calcium channel subunit.
XX
KW   Human calcium channel subunit; diagnosis; agonist; antagonist;
KW   Lambert Eaton syndrome; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             144..6857
FT                   /*tag= a
XX
PN   WO9304083-A.
XX
PD   04-MAR-1993.
XX
PF   14-AUG-1992;   92WO-US06903.
XX
PR   15-AUG-1991;   91US-0745206.
PR   10-APR-1992;   92US-0868354.
XX
PA   (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI   Brenner R,  Ellis SB,  Feldman DH,  Harpold MM,  Mccue AF;
PI   Williams ME;
XX
DR   WPI; 1993-093936/11.
DR   P-PSDB; AAR33550.
XX
PT   DNA encoding specific human calcium channel sub-units - used for
PT   identifying calcium channel agonists and antagonists and
PT   diagnosing Lambert Eaton syndrome
XX
PS   Disclosure; Page 120-128; 150pp; English.
XX
CC   DNA encoding the alpha 1B subunit was isolated by screening a
CC   human basal ganglia cDNA library with  fragments of the rabbit
CC   skeletal muscle calcium channel alpha 1 subunit-encoding cDNA.
CC   A portion of one of the positive clones was used to screen an IMR32
CC   cell cDNA library. Clones that hybridized to the basal ganglia
CC   DNA prove were used to further screen an IMR32 cell cDNA library
CC   to identify overlapping clones that in turn were used to screen a
CC   human hippocampus cDNA library. In this way, a sufficient series of
CC   clones to span nearly the entire length of the nucleotide sequence
CC   encoding the human alpha 1B subunit was obtained. PCR amplification
CC   of specific regions of the IMR32 cell alpha 1B mRNA yielded
CC   additonal segments of the alpha 1B coding sequence. A full-length
CC   alpha 1B DNA clone was constructed by ligating portions of the
CC   partial cDNA clones (see AAQ37817, AAQ37818). Alpha 1B-1 and alpha
CC   1B-2 are derived by alternative splicing of the alpha 1B subunit
CC   transcript.
XX
SQ   Sequence 7175 BP; 1415 A; 2204 C; 2162 G; 1394 T; 0 other;

  Query Match             93.3%;  Score 14;  DB 14;  Length 7175;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCTGCTGAGG 15
           ||||||||||||||
Db    1882 TCCGCCTGCTGAGG 1895


RESULT 14
AAQ84658
ID   AAQ84658 standard; DNA; 7175 BP.
XX
AC   AAQ84658;
XX
```

```
DT   01-DEC-1995  (first entry)
XX
DE   Human neuronal calcium channel subunit alpha 1B-2.
XX
KW   Calcium channel subunit; antagonist; agonist; diagnosis;
KW   Lambert Eaton Syndrome; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             144..6857
FT                   /*tag=  a
FT   misc_feature    6633..7175
FT                   /*tag=  b
FT                   /note= "identical to alpha 1B-1"
XX
PN   WO9504822-A.
XX
PD   16-FEB-1995.
XX
PF   11-AUG-1994;   94WO-US09230.
XX
PR   11-AUG-1993;   93US-0105536.
PR   05-NOV-1993;   93US-0149097.
XX
PA   (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI   Ellis SB,  Gillespie A,  Harpold MM,  Mccue AF,  Williams ME;
XX
DR   WPI; 1995-090900/12.
DR   P-PSDB; AAR71006.
XX
PT   DNA encoding human calcium channel sub-unit(s) - used for
PT   developing prods. for studying calcium channels, e.g. for
PT   obtaining agonists and antagonists
XX
PS   Disclosure; Page 149-160; 285pp; English.
XX
CC   DNA encoding the alpha 1B subunit was isolated by screening a
CC   human basal ganglia cDNA library with fragments of the rabbit
CC   skeletal muscle calcium channel alpha 1 subunit-encoding cDNA.
CC   A portion of one of the positive clones was used to screen an
CC   IMR32 cell cDNA library. Clones that hybridised to the basal
CC   ganglia probe were used to further screen an IMR32 cell cDNA
CC   library to identify overlapping clones that in turn were used
CC   to screen a human hippocampus cDNA libary. A series of clones
CC   to span nearly the entire length of the nt. sequence encoding
CC   the human alpha 1B subunit was obtd. Nucleic acid amplification
CC   of specific regions of the IMR32 cell alpha 1B mRNA yielded
CC   additional segments of the alpha 1B coding sequence. A full-
CC   length alpha 1B DNA clone was constructed by ligating portions
CC   of the partial cDNA clones. Nucleic acid amplification analysis
CC   of IMR32 cell RNA and genomic DNA using oligo primers corresp. to
CC   sequences located 5' and 3' of the stop codon of the DNA encoding
CC   the alpha 1B subunit revealed an alternatively spliced alpha
CC   1B-encoding mRNA in IMR32 cells. This second mRNA product is the
CC   result of differential splicing of the alpha 1B subunit transcript
CC   to include another exon that is not present in the mRNA corresp.
CC   to the other 3' alpha 1B cDNA sequence that was initially isolated.
CC   The alpha 1B subunit encoded by a DNA sequence contg. an additional
CC   exon is referred to as alpha 1B-1 and given in AAQ84657/R71005,
CC   whereas the other form is referred to as alpha 1B-2 and is given in
CC   AAQ84658/R71006. Following the sequence of the additional exon in
CC   alpha 1B-1 the alpha 1B-1 and alpha 1B-2 seuences are identical.
XX
SQ   Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 other;

  Query Match             93.3%;  Score 14;  DB 16;  Length 7175;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCTGCTGAGG 15
           ||||||||||||||
Db    1882 TCCGCCTGCTGAGG 1895


RESULT 15
AAV42686
ID   AAV42686 standard; DNA; 7175 BP.
XX
AC   AAV42686;
XX
DT   12-OCT-1998  (first entry)
XX
DE   DNA encoding human calcium channel alpha-1B-1 subunit.
XX
KW   Alpha-1B subunit; human; calcium channel; assay; detection;
KW   characterisation; Lambert Eaton Syndrome; LES; diagnosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..143
FT                   /*tag=  a
FT   CDS             144..6857
FT                   /*tag=  b
FT   3'UTR           6855..7175
FT                   /*tag=  c
XX
PN   US5792846-A.
XX
PD   11-AUG-1998.
XX
PF   31-MAY-1995;   95US-0455543.
XX
PR   04-APR-1994;   94US-0223305.
PR   04-APR-1988;   88US-0176899.
PR   04-APR-1989;   89US-0603751.
PR   04-APR-1989;   89WO-US01408.
PR   20-FEB-1990;   90US-0482384.
PR   30-NOV-1990;   90US-0620250.
PR   15-AUG-1991;   91US-0745206.
PR   31-MAY-1995;   95US-0455543.
XX
PA   (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI   Brenner R,  Ellis SB,  Feldman DH,  Harpold MM,  McCue AF;
PI   Williams ME;
XX
DR   WPI; 1998-456192/39.
DR   P-PSDB; AAW63142.
XX
PT   DNA encoding human calcium channel alpha 1B sub:unit protein -
PT   useful for recombinant production of the channel for screening of
PT   its modulators, and diagnosis of Lambert Eaton Syndrome
XX
PS   Claim 1; Columns 91-106; 166pp; English.
XX
CC   The present sequence encodes the alpha-1B subunit of a human calcium
CC   channel. The present sequence is derived from alternative splicing of
CC   AAV42685. Calcium channels are membrane-spanning, multi-subunit proteins
CC   that allow controlled entry of calcium ions into cells. This leads
CC   to depolarisation events required for muscle contraction. The
CC   recombinant subunit, when expressed with nucleic acids encoding the
CC   complete calcium channel, can be used in assays for the detection and
CC   characterisation of compounds that modulate the channel. The DNA encoding
CC   the subunits can be alternatively spliced when transcribed, giving more
CC   than one form of the protein from the same transcript, each having
CC   slightly different properties. In addition, the reactivity of the alpha 1
CC   subunit with IgG molecules from the serum of an individual with Lambert
CC   Eaton Syndrome (LES) can be used as a diagnostic for the disease.
XX
SQ   Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 other;

  Query Match             93.3%;  Score 14;  DB 19;  Length 7175;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2 TCCGCCTGCTGAGG 15
           ||||||||||||||
Db    1882 TCCGCCTGCTGAGG 1895
```

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Job time : 64.0455 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 13:09:44 ; Search time 62.0455 Seconds
(without alignments)
415.078 Million cell updates/sec

Title: US-09-856-803-5
Perfect score: 15
Sequence: 1 gtccgcccgctgagg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15	100.0	15	21	AAA38786	Human beta2 adrene
2	15	100.0	20	19	AAV30491	Canine beta-2 adre
3	15	100.0	51	22	AAH79739	Human DNA containi
4	15	100.0	230	22	AAH27139	Human beta-2 adren
5	15	100.0	1999	18	AAT93250	Beta-2 adrenalin r
6	15	100.0	2340	21	AAA38784	Human beta2 adrene
7	15	100.0	2679	19	AAV30468	Canine beta-2 adre
8	15	100.0	3451	19	AAV52614	Human beta-2-adren
9	15	100.0	3451	20	AAZ00776	Human beta 2-adren
10	15	100.0	3451	20	AAZ00779	Human beta 2-adren
11	15	100.0	3451	20	AAZ00773	Human beta 2-adren
12	15	100.0	3451	21	AAA38339	Human beta-adrener
13	15	100.0	3451	24	AAS18444	Reference sequence
14	14	93.3	352	21	AAF10262	Fusarium venenatum
15	14	93.3	2360	23	ABL17700	Drosophila melanog
c 16	14	93.3	2432	21	AAF17997	Lung cancer associ
c 17	14	93.3	2434	23	ABL17701	Drosophila melanog
18	14	93.3	2990	23	ABL26048	Drosophila melanog
19	14	93.3	5548	23	ABL07742	Drosophila melanog
c 20	14	93.3	6153	20	AAV74156	Human mature von W
c 21	14	93.3	6153	20	AAV08901	Von Willebrand fac
c 22	14	93.3	6153	21	AAZ56177	Human von Willebra
c 23	14	93.3	8575	19	AAV18886	Homo sapiens von W
c 24	14	93.3	8585	7	AAN60404	Sequence encoding
c 25	14	93.3	8679	22	AAH57453	Human lung cell sp
c 26	14	93.3	8836	22	AAH98395	Human EST-derived
c 27	14	93.3	9896	23	AAS74631	DNA encoding novel
28	13.4	89.3	15	21	AAA38787	Human beta2 adrene
29	13.4	89.3	741	21	AAA64409	Open reading frame
30	13.4	89.3	746	21	AAZ52371	Human beta-amyloid
31	13.4	89.3	844	17	AAT44381	Calcium channel is
c 32	13.4	89.3	1007	17	AAT34278	Manganese superoxi
c 33	13.4	89.3	1008	14	AAQ63914	MnSOD DNA (exons 1
c 34	13.4	89.3	1325	22	ABA08818	Human secreted pro
35	13.4	89.3	1400	18	AAT93249	Beta-2 adrenalin r
36	13.4	89.3	1473	21	AAA64408	DNA encoding a hum
37	13.4	89.3	1473	21	AAA64424	DNA encoding a hum
38	13.4	89.3	1473	21	AAA64425	DNA encoding a hum
39	13.4	89.3	1473	21	AAA64426	DNA encoding a hum
40	13.4	89.3	1803	23	AAS85124	DNA encoding novel
41	13.4	89.3	2215	22	AAK52115	Human polynucleoti
42	13.4	89.3	2246	22	AAK53099	Human polynucleoti
43	13.4	89.3	2300	20	AAX61116	Human beta2-adrene
44	13.4	89.3	2305	21	AAA38340	Human beta-adrener
c 45	13.4	89.3	2626	9	AAN81159	Human manganese su

ALIGNMENTS

RESULT 1
AAA38786
ID AAA38786 standard; DNA; 15 BP.
XX
AC AAA38786;
XX
DT 05-OCT-2000 (first entry)
XX
DE Human beta2 adrenergic receptor beta2AR C allele-specific probe.
XX
KW Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW congestive heart failure; ischemic heart disease; arrhythmia;
KW obesity; diabetes; vascular disease; premature labour; migraine;
KW anaphylaxis; chronic obstructive pulmonary disease;
KW allele-specific oligonucleotide probe; ss.
XX
OS Homo sapiens.
XX
PN WO200031307-A1.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US27963.
XX
PR 25-NOV-1998; 98US-0109886.
XX
PA (UYCI-) UNIV CINCINNATI.
XX
PI Liggett SB;
XX
DR WPI; 2000-400107/34.

XX
PT Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT receptor (beta 2 AR), useful for predicting genetic disposition to a
PT disease modified by beta 2 AR expression e.g. congestive heart failure,
PT hypertension -
XX
PS Claim 5; Page 11; 56pp; English.
XX
CC The present sequence is an allele-specific oligonucleotide probe
CC for the C allele of the human beta2 adrenergic receptor (beta2AR) gene,
CC which is located on chromosome 5q31 (12). The gene has two different
CC alleles, and it has been shown that the presence of two copies of the T
CC allele leads to higher expression of the gene. This is because the
CC polymorphism is found in the 5' leader sequence, which encodes a peptide
CC which regulates expression of the beta2AR gene. The polymorphism is
CC thought to affect individuals' responses to beta-agonists and
CC beta-antagonists, and is likely to influence their predisposition to
CC asthma, hypertension, congestive heart failure, ischemic heart disease,
CC arrhythmia, obesity, diabetes, vascular disease, premature labour,
CC migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD).
CC The gene can, therefore, be used to predict the susceptibility of an
CC individual to these diseases and determine the best treatment.
XX
SQ Sequence 15 BP; 1 A; 6 C; 6 G; 2 T; 0 other;

Query Match 100.0%; Score 15; DB 21; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCCGCTGAGG 15
||||||||||||||||
Db 1 GTCCGCCCGCTGAGG 15

RESULT 2
AAV30491
ID AAV30491 standard; DNA; 20 BP.
XX
AC AAV30491;
XX
DT 14-OCT-1998 (first entry)
XX
DE Canine beta-2 adrenergic receptor sense primer #1.
XX
KW Canine; beta-adrenergic receptor; brown adipose tissue; probe; human;
KW hybridisation; ligand; primer; ss.
XX
OS Synthetic.
OS Canis familiaris.
XX
PN WO9735973-A2.
XX
PD 02-OCT-1997.
XX
PF 26-MAR-1997; 97WO-FR00537.
XX
PR 26-MAR-1996; 96FR-0003730.
XX
PA (VETI-) VETIGEN.
XX
PI Drumare MF, Lenzen G, Pietri-Rouxel F, Strosberg AD;
XX
DR WPI; 1998-032136/03.
XX
PT Canine beta 2 and beta 3 adrenergic receptors and coding sequences -
PT useful for identifying specific ligands and (ant)agonists to develop
PT specific treatments for obesity in dogs
XX
PS Claim 17; Page 55; 79pp; French.
XX
CC Primers AAV30491-V30510 were used for sequencing the coding region of
CC the canine beta 2-adrenergic receptor (RA-Ca-b2) gene (AAV30468). The
CC beta-2 receptor can be used in comparative structure-function studies,
CC e.g. for differential screening of ligands specific for RA-Ca-b2 or
CC RA-Ca-b3 (AAW44933).
XX
SQ Sequence 20 BP; 2 A; 8 C; 8 G; 2 T; 0 other;

Query Match 100.0%; Score 15; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCCGCTGAGG 15
||||||||||||||||
Db 6 GTCCGCCCGCTGAGG 20

RESULT 3
AAH79739
ID AAH79739 standard; DNA; 51 BP.
XX
AC AAH79739;
XX
DT 19-SEP-2001 (first entry)
XX
DE Human DNA containing single nucleotide polymorphism SEQ ID NO. 354.
XX
KW Human; single nucleotide polymorphism; SNP; angiopoietin;
KW 4-hydroxybutyrate; dehydrogenase; protein therapy;
KW adenosine triphosphate-dependent RNA helicase;
KW major histocompatibility complex Class I histocompatibility antigen; MHC;
KW phosphoglycerate kinase; immunosuppressive; immunostimulatory;
KW antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
KW antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200148245-A2.
XX
PD 05-JUL-2001.
XX
PF 27-DEC-2000; 2000WO-US35346.
XX
PR 27-DEC-1999; 99US-0472688.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-418297/44.
XX
PT Polymorphic nucleic acids encoding e.g. angiopoietin, dehydrogenase,
PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
PT diseases and infections -
XX
PS Claim 1; Page 162; 484pp; English.
XX
CC The invention relates to nucleic acids (AAH79386-AAH80036) encoding
CC polymorphic variants of proteins (AAG98010-AAG98238) related to
CC angiopoietin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
CC proteins have potential immunosuppressive, immunostimulatory,
CC antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
CC antileukemic, neuroprotective and antimicrobial activity and may be
CC useful in gene/protein therapy, vaccines, modulation of the expression
CC and activity of proteins related to angiopoietin, 4-hydroxybutyrate,
CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase,
CC major histocompatibility complex (MHC) Class I histocompatibility antigen
CC and/or phosphoglycerate kinase. Disorders that may be prevented,
CC diagnosed and/or treated by the above methods include multifactorial
CC diseases with a genetic component, such as autoimmune diseases (e.g.
CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
CC erytheromatosus and Grave's disease), inflammation, cancer (e.g. cancers

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CC   of the bladder, brain, breast, colon and kidney, leukemia), diseases of
CC   the nervous system, an infection of pathogenic organisms. They may also
CC   be used to alter phenotypic traits such as longevity, appearance,
CC   strength, speed and endurance.
XX
SQ   Sequence 51 BP; 5 A; 24 C; 18 G; 4 T; 0 other;

  Query Match            100.0%;  Score 15;  DB 22;  Length 51;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db     19 GTCCGCCCGCTGAGG 33


RESULT 4
AAH27139
ID   AAH27139 standard; DNA; 230 BP.
XX
AC   AAH27139;
XX
DT   08-AUG-2001  (first entry)
XX
DE   Human beta-2 adrenergic receptor UTR region with RBP binding ability.
XX
KW   Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration;
KW   stroke; cardiovascular disease; hypertension; cancer; inflammation;
KW   metabolic disorder; obesity; diabetes; beta-2 adrenergic receptor; ds.
XX
OS   Homo sapiens.
XX
PN   WO200134624-A1.
XX
PD   17-MAY-2001.
XX
PF   09-NOV-2000; 2000WO-US30888.
XX
PR   10-NOV-1999;   99US-0437458.
XX
PA   (MESS-) MESSAGE PHARM INC.
XX
PI   Giordano A,  Xavier AK;
XX
DR   WPI; 2001-335904/35.
XX
PT   New nucleic acids that bind RNA-binding proteins or regulate mRNA
PT   function, useful for therapeutic gene regulation, such as in cases of
PT   neurodegeneration  -
XX
PS   Claim 1; Page 28; 33pp; English.
XX
CC   Sequences AAH27132 - AAH27151 represent human gene untranslated regions
CC   where the corresponding mRNA fragment has RNA binding protein (RBP)
CC   binding activity. RBPs mediate the processing of pre-mRNA, the transport
CC   of mRNA from the nucleus to the cytoplasm, mRNA stabilisation,
CC   translational efficiency, and the sequestration of some mRNAs. Therefore
CC   modification of post-transcriptional protein expression in eukaryotic
CC   cells may be carried out through the targeting specific interactions of
CC   proteins that bind to RBPs. The gene fragments of the invention are used
CC   to identify their optimized sub-fragments, compounds that affect RNA/RBP
CC   interaction or mRNA functionality; or RBPs that interact with the
CC   compounds. Compounds identified using the gene fragments are potentially
CC   useful for therapeutic regulation of gene expression, such as in cases of
CC   neurodegeneration; stroke; cardiovascular disease; hypertension; cancer;
CC   inflammation; metabolic disorders (obesity and diabetes) and bacterial or
CC   viral infection. The present sequence is one of gene fragments of the
CC   invention, isolated from the human beta-2 adrenergic receptor gene.
XX
SQ   Sequence 230 BP; 42 A; 91 C; 70 G; 27 T; 0 other;

  Query Match            100.0%;  Score 15;  DB 22;  Length 230;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db    166 GTCCGCCCGCTGAGG 180


RESULT 5
AAT93250
ID   AAT93250 standard; cDNA to mRNA; 1999 BP.
XX
AC   AAT93250;
XX
DT   20-APR-1998  (first entry)
XX
DE   Beta-2 adrenalin receptor subtype coding sequence.
XX
KW   Beta-2 adrenalin subtype; cyanopindrol; agonist; antagonist;
KW   asthmatic disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             190..1431
FT                   /*tag=  a
XX
PN   WO9735963-A1.
XX
PD   02-OCT-1997.
XX
PF   24-MAR-1997;   97WO-JP00982.
XX
PR   27-MAR-1996;   96JP-0072914.
XX
PA   (DAIN ) DAINIPPON PHARM CO LTD.
XX
PI   Fujii K,  Furutani Y,  Kawashima H,  Nomura A,  Yano K;
XX
DR   WPI; 1997-489627/45.
DR   P-PSDB; AAW34320.
XX
PT   Novel beta-2 adrenalin receptor sub-type - useful for screening for
PT   agonists and antagonists and researching asthmatic diseases
XX
PS   Disclosure; Page 27-30; 47pp; Japanese.
XX
CC   This sequence encodes the protein of the invention. The protein of the
CC   invention is a beta-2 adrenalin receptor subtype with Kd value of
CC   approximately 75 pM against 125I-cyanopindrol. The protein can be used in
CC   screening for agonists and antagonists, which are useful in researching
CC   asthmatic diseases.
XX
SQ   Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T; 0 other;

  Query Match            100.0%;  Score 15;  DB 18;  Length 1999;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db    136 GTCCGCCCGCTGAGG 150


RESULT 6
AAA38784
ID   AAA38784 standard; DNA; 2340 BP.
XX
AC   AAA38784;
XX
DT   05-OCT-2000  (first entry)
XX
DE   Human beta2 adrenergic receptor beta2AR gene.
XX
```

```
KW   Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW   chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW   congestive heart failure; ischemic heart disease; arrhythmia;
KW   obesity; diabetes; vascular disease; premature labour; migraine;
KW   anaphylaxis; chronic obstructive pulmonary disease; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1487..2340
FT                   /*tag= a
FT                   /product= "beta2 adrenergic receptor"
FT                   /note= "no stop codon given at 3' end of sequence"
FT                   /partial
FT   sig_peptide     1487..1546
FT                   /*tag= b
FT                   /label= 5'_leader_cistron
FT   allele          replace(1541,T)
FT                   /*tag= c
FT   mat_peptide     1588..2340
FT                   /*tag= d
XX
PN   WO200031307-A1.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US27963.
XX
PR   25-NOV-1998;   98US-0109886.
XX
PA   (UYCI-) UNIV CINCINNATI.
XX
PI   Liggett SB;
XX
DR   WPI; 2000-400107/34.
XX
PT   Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT   receptor (beta 2 AR), useful for predicting genetic disposition to a
PT   disease modified by beta 2 AR expression e.g. congestive heart failure,
PT   hypertension -
XX
PS   Disclosure; Figure 1; 56pp; English.
XX
CC   The present sequence is a fragment of the C allele of the human beta2
CC   adrenergic receptor (beta2AR) gene, which is located on chromosome
CC   5q31 (12). The gene has two different alleles, and it has been shown that
CC   the presence of two copies of the T allele leads to higher expression of
CC   the gene. This is because the polymorphism is found in the 5' leader
CC   sequence, which encodes a peptide which regulates expression of the
CC   beta2AR gene. The polymorphism is thought to affect individuals'
CC   responses to beta-agonists and beta-antagonists, and is likely to
CC   influence their predisposition to asthma, hypertension,
CC   congestive heart failure, ischemic heart disease, arrhythmia, obesity,
CC   diabetes, vascular disease, premature labour, migraine, anaphylaxis and
CC   chronic obstructive pulmonary disease (COPD). The gene can, therefore, be
CC   used to predict the susceptibility of an individual to these diseases and
CC   determine the best treatment.
XX
SQ   Sequence 2340 BP; 498 A; 627 C; 653 G; 562 T; 0 other;

  Query Match             100.0%;  Score 15;  DB 21;  Length 2340;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db    1534 GTCCGCCCGCTGAGG 1548


RESULT 7
AAV30468
ID   AAV30468 standard; cDNA to mRNA; 2679 BP.
XX
AC   AAV30468;
XX
DT   14-OCT-1998  (first entry)
XX
DE   Canine beta-2 adrenergic receptor coding sequence.
XX
KW   Canine; beta-adrenergic receptor; brown adipose tissue; probe; human;
KW   hybridisation; ligand; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             169..1416
FT                   /*tag= a
FT                   /product= "beta-2 adrenergic receptor"
XX
PN   WO9735973-A2.
XX
PD   02-OCT-1997.
XX
PF   26-MAR-1997;   97WO-FR00537.
XX
PR   26-MAR-1996;   96FR-0003730.
XX
PA   (VETI-) VETIGEN.
XX
PI   Drumare MF,  Lenzen G,  Pietri-Rouxel F,  Strosberg AD;
XX
DR   WPI; 1998-032136/03.
DR   P-PSDB; AAW44932.
XX
PT   Canine beta 2 and beta 3 adrenergic receptors and coding sequences -
PT   useful for identifying specific ligands and (ant)agonists to develop
PT   specific treatments for obesity in dogs
XX
PS   Claim 1; Page 45-46; 79pp; French.
XX
CC   This sequence represent the coding region of the canine beta
CC   2-adrenergic receptor (RA-Ca-b2) gene.  The sequence was isolated from a
CC   cDNA library constructed from polyA+ RNA purified from dog brown adipose
CC   tissue cells. The probe was a 600 bp fragment of the coding region of the
CC   human beta-3 adrenergic receptor covering the region from the initiation
CC   codon to transmembrane domain 5 (TM5).  The full length insert was cloned
CC   into M13 for sequencing using primers AAV30491-V30510.  The sequence can
CC   then be expressed e.g. in a mammalian cell, by subcloning into an
CC   expression vector such as pCDNA3.  The beta-2 receptor can be used in
CC   comparative structure-function studies, e.g. for differential screening
CC   of ligands specific for RA-Ca-b2 or RA-Ca-b3 (AAW44933).
XX
SQ   Sequence 2679 BP; 577 A; 736 C; 724 G; 642 T; 0 other;

  Query Match             100.0%;  Score 15;  DB 19;  Length 2679;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db     122 GTCCGCCCGCTGAGG 136


RESULT 8
AAV52614
ID   AAV52614 standard; cDNA; 3451 BP.
XX
AC   AAV52614;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Human beta-2-adrenergic receptor cDNA.
XX
KW   Beta-2-adrenergic receptor; human; asthma; beta-agonist;
KW   polymorphism; ds.
XX
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OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1588..2829
FT                   /*tag= a
FT   variation       1633
FT                   /*tag= b
FT                   /note= "A to G substitution, results in Arg16
FT                          to Gly amino acid change"
XX
PN   WO9839477-A2.
XX
PD   11-SEP-1998.
XX
PF   26-FEB-1998;   98WO-US03908.
XX
PR   03-MAR-1997;   97US-0811441.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Boushey H,  Chinchilli VM,  Drazen JM,  Fish JE,  Ford JG;
PI   Martin RJ;
XX
DR   WPI; 1998-506372/43.
DR   P-PSDB; AAW75777.
XX
PT   Diagnosing asthma patients predisposed to adverse beta-agonist
PT   reactions upon regular administration - by identifying patients
PT   homozygous for allele encoding Arg at position 16 of
PT   beta2-adrenergic receptor protein
XX
PS   Disclosure; Page 33-35; 46pp; English.
XX
CC   This cDNA sequence codes for human beta-2-adrenergic receptor (see
CC   AAW75777) having an arginine residue at position 16.  A novel method
CC   for identifying individuals susceptible to adverse responses to
CC   regular administration of beta-agonists comprises: (a) identifying
CC   in a genomic nucleic acid sample from the individual first and
CC   second alleles of the beta 2-adrenergic receptor gene, and (b)
CC   classifying an individual as susceptible if first and second
CC   alleles both encode Arg at residue 16 of the beta 2-adrenergic
CC   receptor protein.  Beta 2-adrenergic receptor gene alleles may be
CC   identified by any known method e.g. denaturing gel electrophoresis
CC   or PCR amplification (see also AAV52615-17).  Identification
CC   preferably comprises amplifying a portion of each allele which
CC   includes the sequence encoding residue 16, and optionally also
CC   comprises determining nucleotide sequences of these portions (e.g.
CC   by automated sequence analysis).  The invention identifies a known
CC   polymorphism in the beta 2-adrenergic receptor gene as being linked
CC   to adverse responses to regular beta-agonist administration;
CC   position 16 of the encoded protein can be either Arg or Gly, and
CC   individuals homozygous for Arg16 are more susceptible.
XX
SQ   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

  Query Match             100.0%;  Score 15;  DB 19;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db    1534 GTCCGCCCGCTGAGG 1548


RESULT 9
AAZ00776
ID   AAZ00776 standard; DNA; 3451 BP.
XX
AC   AAZ00776;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 3.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1633,a)
FT                   /*tag= a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
FT   mutation        replace(1666,c)
FT                   /*tag= b
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Glu
FT                          residue to Gln residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 4; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 789 A; 872 C; 897 G; 893 T; 0 other;

  Query Match             100.0%;  Score 15;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
```

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels     );  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db    1534 GTCCGCCCGCTGAGG 1548


RESULT 10
AAZ00779
ID   AAZ00779 standard; DNA; 3451 BP.
XX
AC   AAZ00779;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 6.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1568,t)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1633,a)
FT                   /*tag=  b
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
FT   mutation        replace(1666,c)
FT                   /*tag=  c
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Glu
FT                          residue to Gln residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 7; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 789 A; 873 C; 897 G; 892 T; 0 other;

  Query Match             100.0%;  Score 15;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db    1534 GTCCGCCCGCTGAGG 1548


RESULT 11
AAZ00773
ID   AAZ00773 standard; DNA; 3451 BP.
XX
AC   AAZ00773;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor wild type DNA.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(159,a)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation        replace(245,g)
FT                   /*tag=  b
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation        replace(565,a)
FT                   /*tag=  c
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation        replace(934,a)
FT                   /*tag=  d
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation        replace(1120,c)
FT                   /*tag=  e
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation        replace(1221,t)
FT                   /*tag=  f
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
```

```
FT   AAZ00774" mutation        replace(1541,t)
FT                  /*tag=  g
FT                  /note= "This mutation results in a change in the
FT                         corresponding wild type amino acid sequence
FT                         from an Arg residue to Cys residue in the
FT                         variant sequences represented in AAZ00774,
FT                         AAZ00775, AAZ00777, AAZ00778 and AAZ00780"
FT   mutation        replace(1568,c)
FT                  /*tag=  h
FT                  /note= "This nucleotide differs from the wild type
FT                         in the variant nucleotide sequences represented
FT                         in AAZ00774 and AAZ00779"
FT   mutation        replace(1633,g)
FT                  /*tag=  i
FT                  /note= "This mutation results in a change in the
FT                         corresponding wild type amino acid sequence
FT                         from an Arg residue to Gly residue in the
FT                         variant sequences represented in AAZ00774,
FT                         AAZ00776, AAZ00777, AAZ00779 and AAZ00780"
FT   mutation        replace(1666,g)
FT                  /*tag=  j
FT                  /note= "This mutation results in a change in the
FT                         corresponding wild type amino acid sequence
FT                         from a Gln residue to Glu residue in the
FT                         variant sequences represented in AAZ00774,
FT                         AAZ00776, AAZ00779"
FT   mutation        replace(1839,a)
FT                  /*tag=  k
FT                  /note= "This nucleotide differs from the wild type
FT                         sequence in the sequence represented in
FT   AAZ00774" mutation        replace(2078,t)
FT                  /*tag=  l
FT                  /note= "This mutation results in a change in the
FT                         corresponding wild type amino acid sequence
FT                         from a Thr residue to Ile residue"
FT   mutation        replace(2110,a)
FT                  /*tag=  m
FT                  /note= "This nucleotide differs from the wild type
FT                         sequence in the sequence represented in
FT   AAZ00774" mutation        replace(2640,c)
FT                  /*tag=  n
FT                  /note= "This nucleotide differs from the wild type
FT                         sequence in the sequence represented in
FT   AAZ00774" mutation        replace(2826,a)
FT                  /*tag=  o
FT                  /note= "This nucleotide differs from the wild type
FT                         sequence in the sequence represented in
FT                         AAZ00774"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Disclosure; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be determined
CC   include neuropsychiatric disease, such as depression, anxiety, attention
CC   deficit disorder with hyperactivity, eating disorders, e.g. anorexia
CC   nervosa and bulimia, or post-traumatic stress disorder. Diseases of the
CC   autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and
CC   Riley-Day syndromes having selective noradrenergic-receptor disposition,
CC   or migraine, allergic conditions, e.g. asthma and atopic disorders, and
CC   metabolic illnesses, e.g. morbid obesity including predicting a change in
CC   weight, using body mass index, can also be determined. The beta
CC   2-adrenergic receptor sequence variants can be used to develop
CC   therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor
CC   agonists can be developed. Treatments can be optimized for individuals,
CC   including gene therapy and pharmaceutical intervention therapy. This
CC   sequence represents the wild type human beta 2-adrenergic receptor
CC   gene which is described in the method of the invention.
XX
SQ   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

  Query Match             100.0%;  Score 15;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db    1534 GTCCGCCCGCTGAGG 1548


RESULT 12
AAA38339
ID   AAA38339 standard; DNA; 3451 BP.
XX
AC   AAA38339;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human beta-adrenergic receptor-2 gene regulatory region.
XX
KW   Beta-adrenergic receptor-2 gene; regulatory region;
KW   polymorphism; polymorphic marker; cardiovascular disease;
KW   myocardial infarction; unstable angina; hypertension; atherosclerosis;
KW   stroke; prognosis; drug screening; treatment outcome; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO200022166-A2.
XX
PD   20-APR-2000.
XX
PF   13-OCT-1999;   99WO-IB01678.
XX
PR   14-OCT-1998;   98US-0104286.
PR   14-OCT-1998;   98US-0104302.
XX
PA   (EURO-) EURONA MEDICAL AB.
XX
PI   Norberg LT,  Andersson MK,  Lindstrom PHR,  Jonsson L;
XX
DR   WPI; 2000-318010/27.
XX
PT   Assessing cardiovascular status in humans involves comparing test
PT   polymorphic pattern comprising polymorphic positions within genes
PT   encoding specific proteins, with reference polymorphic pattern -
XX
PS   Disclosure; Page 123-124; 126pp; English.
XX
CC   The invention relates to a novel method of assessing the cardiovascular
CC   status in an individual and to newly identified polymorphisms in the
CC   genes encoding angiotensin-converting enzyme (ACE), angiotensin II
CC   receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
CC   aldosterone synthase, endothelin receptor type A and beta-adrenergic
CC   receptors 1 and 2. The method comprises determining the sequence at one
CC   or more polymorphic positions within these genes, and comparing the
CC   pattern of polymorphisms from the individual with a reference polymorphic
```

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CC   pattern obtained from a population of individuals exhibiting a
CC   predetermined cardiovascular disease status. The polymorphic markers are
CC   useful for determining the predisposition of an individual to
CC   cardiovascular disorders such as myocardial infarction, unstable angina,
CC   hypertension, atherosclerosis and stroke. They are also useful for
CC   predicting the likely cardiovascular status of a patient given a
CC   treatment regimen comprising administration of cardiovascular drugs
CC   (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
CC   blockers) or calcium channel blockers). One or more polymorphic markers
CC   provides a basis for predicting the outcome of a treatment regimen.
CC   Fragments of the genes comprising a polymorphic site may be used as
CC   primers and probes for detecting genetic polymorphisms or in molecular
CC   library arrays for high throughput screening. The genes, and the proteins
CC   they encode are useful in the screening of potential cardiovascular
CC   drugs. Determination of an individual's polymorphic pattern reduces or
CC   eliminates trial and error in selecting a treatment for a particular
CC   individual cardiovascular patient. It also provides the ability to
CC   eliminate patients from clinical trials who are predicted to be
CC   non-responsive, or at a risk for an adverse response, to a particular
CC   treatment regimen. Adverse results in an early trial can be evaluated to
CC   identify polymorphic patterns so that the adverse results can be
CC   correlated with a sub-population of the test population, permitting
CC   exclusion of such sub-populations from the treatment group. Beneficial
CC   drugs can be approved for use in the appropriate population, thereby
CC   decreasing the number of patients required for a clinical trial, which in
CC   turn decreases the duration and cost of such trials. The present
CC   sequence represents the human beta-adrenergic receptor-2 gene
CC   regulatory region (GenBank M15169, J02728, M16106). The polymorphic
CC   sites identified are 934A/G, 987C/G, 1006A/G, 1120C/G, 1221C/T,
CC   1541C/T and 1568C/T.
XX
SQ   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

  Query Match             100.0%;  Score 15;  DB 21;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db    1534 GTCCGCCCGCTGAGG 1548


RESULT 13
AAS18444
ID   AAS18444 standard; DNA; 3451 BP.
XX
AC   AAS18444;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Reference sequence for human beta2AR gene showing polymorphisms.
XX
KW   Human; beta2-adrenergic receptor; beta2AR polymorphism; asthma;
KW   chromosome 5q31-32; migraine; congestive heart failure; hypertension;
KW   ischaemic heart disease; chronic obstructive pulmonary disease; COPD;
KW   obesity; diabetes mellitus; premature labour; vasotropic; cardiant;
KW   antiarrhythmic; antiasthmatic; antidiabetic; tocolytic; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace (565, A)
FT                   /*tag= a
FT                   /note= "Polymorphic site 1 (PS1)"
FT   variation       replace (879, A)
FT                   /*tag= b
FT                   /note= "Polymorphic site 2 (PS2)"
FT   variation       replace (934, A)
FT                   /*tag= c
FT                   /note= "Polymorphic site 3 (PS3)"
FT   variation       replace (1120, C)
FT                   /*tag= d
FT                   /note= "Polymorphic site 4 (PS4)"
FT   variation       replace (1182, T)
FT                   /*tag= e
FT                   /note= "Polymorphic site 5 (PS5)"
FT   variation       replace (1221, T)
FT                   /*tag= f
FT                   /note= "Polymorphic site 6 (PS6)"
FT   variation       replace (1541, T)
FT                   /*tag= g
FT                   /note= "Polymorphic site 7 (PS7)"
FT   variation       replace (1568, C)
FT                   /*tag= h
FT                   /note= "Polymorphic site 8 (PS8)"
FT   CDS             1588..2829
FT                   /*tag= i
FT                   /product= "Beta2AR"
FT   variation       replace (1633, G)
FT                   /*tag= j
FT                   /note= "Polymorphic site 9 (PS9)"
FT   variation       replace (1666, G)
FT                   /*tag= k
FT                   /note= "Polymorphic site 10 (PS10)"
FT   variation       replace (1839, A)
FT                   /*tag= l
FT                   /note= "Polymorphic site 11 (PS11)"
FT   variation       replace (2078, T)
FT                   /*tag= m
FT                   /note= "Polymorphic site 12 (PS12)"
FT   variation       replace (2110, A)
FT                   /*tag= n
FT                   /note= "Polymorphic site 13 (PS13)"
XX
PN   WO200179252-A1.
XX
PD   25-OCT-2001.
XX
PF   13-APR-2000; 2000WO-US10125.
XX
PR   13-APR-2000; 2000WO-US10125.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
PA   (UYCI-) UNIV CINCINNATI.
XX
PI   Stack CB,  Drysdale CM,  Stephens JC,  Nandabalan K,  Judson RS;
PI   Liggett SB;
XX
DR   WPI; 2002-061968/08.
DR   P-PSDB; AAU10763.
XX
PT   New isolated beta 2-adrenergic receptor polynucleotide, useful for
PT   studying expression and biological function of receptor and for
PT   developing drugs targeting receptor, comprises polymorphism of
PT   adenosine at PS2 and thymine at PS5 -
XX
PS   Claim 1; Fig 1; 67pp; English.
XX
CC   The present invention relates to polymorphisms and haplotypes of
CC   the human beta2-adrenergic receptor (beta2-AR) gene located on
CC   chromosome 5q31-32, and methods for haplotyping and/or genotyping the
CC   beta2AR gene in an individual. The methods of the invention make use of
CC   allele-specific oligonucleotides (ASOs) as probes and primers for
CC   detecting the beta2AR gene polymorphisms. The beta2AR gene polymorphisms
CC   are useful in studying the expression and biological function of beta2AR,
CC   and for developing drugs targeting this receptor. They are also useful
CC   for therapeutic purposes such as treating disorders affected by
CC   expression or function of beta2AR such as congestive heart failure,
CC   arrhythmia, ischaemic heart disease, hypertension, migraine, asthma,
CC   chronic obstructive pulmonary disease (COPD), obesity, diabetes and
CC   premature labour. The method is useful for determining the frequency of
CC   a beta2AR genotype or haplotype in a population. The present sequence
CC   represents a reference sequence for the human beta2AR gene which shows
CC   the polymorphisms in the gene.
XX
SQ   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
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  Query Match             100.0%;  Score 15;  DB 24;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db    1534 GTCCGCCCGCTGAGG 1548


RESULT 14
AAF10262
ID   AAF10262 standard; cDNA; 352 BP.
XX
AC   AAF10262;
XX
DT   13-MAR-2001  (first entry)
XX
DE   Fusarium venenatum EST SEQ ID NO:2785.
XX
KW   Multiple gene expression; filamentous fungal cell; EST;
KW   expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW   Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KW   culture condition; environmental stress; spore morphogenesis;
KW   metabolic pathway engineering; catabolic pathway engineering; ss.
XX
OS   Fusarium venenatum.
XX
PN   WO200056762-A2.
XX
PD   28-SEP-2000.
XX
PF   22-MAR-2000; 2000WO-US07781.
XX
PR   22-MAR-1999;   99US-0273623.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Berka RM,  Rey MW,  Shuster JR,  Kauppinen S,  Clausen IG,  Olsen PB;
XX
DR   WPI; 2000-594572/56.
XX
PT   Monitoring differential expression of genes in filamentous fungal cells
PT   uses fluorescence-labeled nucleic acids isolated from the cells and a
PT   substrate of expressed sequence tags -
XX
PS   Claim 86; Page 1393; 3161pp; English.
XX
CC   The present invention describes a method for monitoring differential
CC   expression of genes in a first filamentous fungal (FF) cell relative to
CC   expression of the same genes in one or more second filamentous fungal
CC   cells. The method uses fluorescence-labeled nucleic acids isolated from
CC   the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC   are used in the methods for monitoring differential expression of genes
CC   in a first filamentous fungal (FF) cell relative to expression of the
CC   same genes in one or more second filamentous fungal cells. Monitoring
CC   the global expression of genes from FF cells allows the production
CC   potential of the microorganisms to be improved. New genes may be
CC   discovered, possible functions of unknown open reading frames can be
CC   identified and gene copy number variation and stability can be
CC   monitored. The expression of genes can be used to study how FF cells
CC   adapt to changes in culture conditions, environmental stress, spore
CC   morphogenesis, recombination, metabolic or catabolic pathway
CC   engineering. Using ESTs provides several advantages over genomic or
CC   random cDNA clones including elimination of redundancy as one spot on an
CC   array equals one gene or open reading frame, and organisation of the
CC   microarrays based on function of the gene products to facilitate
CC   analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC   Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC   niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC   AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
CC   all specifically claimed in the present invention.
XX
SQ   Sequence 352 BP; 114 A; 80 C; 93 G; 65 T; 0 other;

  Query Match             93.3%;  Score 14;  DB 21;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCCGCTGAGG 15
           ||||||||||||||
Db       8 TCCGCCCGCTGAGG 21


RESULT 15
ABL17700
ID   ABL17700 standard; DNA; 2360 BP.
XX
AC   ABL17700;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 4573.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 4573; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2360 BP; 555 A; 620 C; 613 G; 572 T; 0 other;

  Query Match             93.3%;  Score 14;  DB 23;  Length 2360;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Job time : 64.0455 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-856-803-6
Perfect score: 15
Sequence: 1 gtccgcctgctgagg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14	93.3	1100	4	US-08-456-200B-17	Sequence 17, Appl
2	14	93.3	2470	1	US-07-745-206A-14	Sequence 14, Appl
3	14	93.3	2470	2	US-08-311-363-14	Sequence 14, Appl
4	14	93.3	5467	1	US-07-745-206A-12	Sequence 12, Appl
5	14	93.3	5467	2	US-08-311-363-12	Sequence 12, Appl
6	14	93.3	6232	4	US-08-456-200B-11	Sequence 11, Appl
7	14	93.3	7175	1	US-08-455-543A-8	Sequence 8, Appli
8	14	93.3	7175	2	US-08-193-078B-8	Sequence 8, Appli
9	14	93.3	7175	2	US-08-223-305C-8	Sequence 8, Appli
10	14	93.3	7175	2	US-08-149-097D-8	Sequence 8, Appli
11	14	93.3	7175	3	US-08-949-386-8	Sequence 8, Appli
12	14	93.3	7175	3	US-08-450-562-8	Sequence 8, Appli
13	14	93.3	7175	4	US-08-984-709A-8	Sequence 8, Appli
14	14	93.3	7177	4	US-09-268-163-7	Sequence 7, Appli
15	14	93.3	7266	3	US-08-713-118-1	Sequence 1, Appli
16	14	93.3	7266	3	US-09-452-007-1	Sequence 1, Appli
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18	14	93.3	7362	2	US-08-193-078B-7	Sequence 7, Appli
19	14	93.3	7362	2	US-08-223-305C-7	Sequence 7, Appli
20	14	93.3	7362	2	US-08-149-097D-7	Sequence 7, Appli
21	14	93.3	7362	3	US-08-949-386-7	Sequence 7, Appli
22	14	93.3	7362	3	US-08-450-562-7	Sequence 7, Appli
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24	14	93.3	7364	4	US-09-268-163-5	Sequence 5, Appli
25	14	93.3	7376	4	US-09-268-163-3	Sequence 3, Appli
26	14	93.3	10627	1	US-08-060-925A-12	Sequence 12, Appl
27	13.4	89.3	36	1	US-08-291-932A-387	Sequence 387, App
28	13.4	89.3	36	1	US-08-291-932A-565	Sequence 565, App
29	13.4	89.3	36	1	US-08-291-932A-754	Sequence 754, App
30	13.4	89.3	36	2	US-08-292-620A-1339	Sequence 1339, Ap
31	13.4	89.3	36	2	US-08-292-620A-1386	Sequence 1386, Ap
32	13.4	89.3	36	3	US-09-071-845-1339	Sequence 1339, Ap
33	13.4	89.3	36	3	US-09-071-845-1386	Sequence 1386, Ap
34	13.4	89.3	230	4	US-09-437-457-8	Sequence 8, Appli
c 35	13.4	89.3	308	2	US-08-673-190A-4	Sequence 4, Appli
c 36	13.4	89.3	1347	4	US-09-286-529-18	Sequence 18, Appl
37	13.4	89.3	5904	1	US-07-745-206A-6	Sequence 6, Appli
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44	13.4	89.3	6575	3	US-08-450-562-3	Sequence 3, Appli
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ALIGNMENTS

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RESULT 1
US-08-456-200B-17
; Sequence 17, Application US/08456200B
; Patent No. 6229000
;  GENERAL INFORMATION:
;    APPLICANT:  Franz, Jurgen; Weingartner, Bernhard;
;    APPLICANT:  Unterbeck, Axel; Rae, Peter
;    TITLE OF INVENTION:  TISSUE-SPECIFIC HUMAN NEURONAL
;    TITLE OF INVENTION:  CALCIUM CHANNEL SUB-TYPES AND
;    TITLE OF INVENTION:  THEIR USE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SPRUNG HORN KRAMER & WOODS
;      STREET:  660 White Plains Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10591-5144
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MB
;      MEDIUM TYPE:  storage
;      COMPUTER:  NEC Powermate SX/20
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/456,200B
;      FILING DATE:  31-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/094,712
;      FILING DATE:  19-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/858,278
;      FILING DATE:  26-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,778
;      FILING DATE:  19-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 41 10 785
;      FILING DATE:  04-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kurt G. Briscoe
;      REGISTRATION NUMBER:  33,141
;      REFERENCE/DOCKET NUMBER:  Bayer 8398.3-KGB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 332-1700
;      TELEFAX:  (914) 332-1844
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  1100 nucleotides
;      TYPE:  Nucleotide
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA
US-08-456-200B-17

  Query Match             93.3%;  Score 14;  DB 4;  Length 1100;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCGCCTGCTGAGG 15
          ||||||||||||||
Db    906 TCCGCCTGCTGAGG 919


RESULT 2
US-07-745-206A-14
; Sequence 14, Application US/07745206A
; Patent No. 5429921
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Feldman, Daniel
;    TITLE OF INVENTION:  Human Calcium Channel Compositions and
;    TITLE OF INVENTION:  Methods
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitch, Even, Tabin & Flannery
;      STREET:  135 S. LaSalle
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/745,206A
;      FILING DATE:  19910815
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Feder, Scott B
;      REFERENCE/DOCKET NUMBER:  51504
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-372-7842
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2470 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2469
US-07-745-206A-14

  Query Match             93.3%;  Score 14;  DB 1;  Length 2470;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCGCCTGCTGAGG 15
          ||||||||||||||
Db   1739 TCCGCCTGCTGAGG 1752


RESULT 3
US-08-311-363-14
; Sequence 14, Application US/08311363
; Patent No. 5876958
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  Human Calcium Channel Compositions and
;    TITLE OF INVENTION:  Methods
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/311,363
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/745,206
;      FILING DATE:  15-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-51506
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2470 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2469
US-08-311-363-14

  Query Match             93.3%;  Score 14;  DB 2;  Length 2470;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCGCCTGCTGAGG 15
          ||||||||||||||
Db   1739 TCCGCCTGCTGAGG 1752


RESULT 4
US-07-745-206A-12
; Sequence 12, Application US/07745206A
; Patent No. 5429921
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Feldman, Daniel
;    TITLE OF INVENTION:  Human Calcium Channel Compositions and
;    TITLE OF INVENTION:  Methods
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitch, Even, Tabin & Flannery
```

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;      STREET:  135 S. LaSalle
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/745,206A
;      FILING DATE:  19910815
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Feder, Scott B
;      REFERENCE/DOCKET NUMBER:  51504
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-372-7842
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5467 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(144..3164, 3168..3245, 3249..3386, 3390
;      LOCATION:  ..3392, 3396..3488, 3495..3539, 3543..3581, 3585
;      LOCATION:  ..3587, 3591..3626, 3630..3689, 3693..3737, 3744
;      LOCATION:  ..3746, 3750..4823, 4827..4841, 4845..5006, 5010
;      LOCATION:  ..5096, 5100..5306, 5310..5366, 5370..5465)
US-07-745-206A-12

  Query Match             93.3%;  Score 14;  DB 1;  Length 5467;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCGCCTGCTGAGG 15
          ||||||||||||||
Db   1882 TCCGCCTGCTGAGG 1895


RESULT 5
US-08-311-363-12
; Sequence 12, Application US/08311363
; Patent No. 5876958
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  Human Calcium Channel Compositions and
;    TITLE OF INVENTION:  Methods
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/311,363
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/745,206
;      FILING DATE:  15-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-51506
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5467 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(144..3164, 3168..3245, 3249..3386, 3390
;      LOCATION:  ..3392, 3396..3488, 3495..3539, 3543..3581, 3585
;      LOCATION:  ..3587, 3591..3626, 3630..3689, 3693..3737, 3744
;      LOCATION:  ..3746, 3750..4823, 4827..4841, 4845..5006, 5010
;      LOCATION:  ..5096, 5100..5306, 5310..5366, 5370..5465)
US-08-311-363-12

  Query Match             93.3%;  Score 14;  DB 2;  Length 5467;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCGCCTGCTGAGG 15
          ||||||||||||||
Db   1882 TCCGCCTGCTGAGG 1895


RESULT 6
US-08-456-200B-11
; Sequence 11, Application US/08456200B
; Patent No. 6229000
;  GENERAL INFORMATION:
;    APPLICANT:  Franz, Jurgen; Weingartner, Bernhard;
;    APPLICANT:  Unterbeck, Axel; Rae, Peter
;    TITLE OF INVENTION:  TISSUE-SPECIFIC HUMAN NEURONAL
;    TITLE OF INVENTION:  CALCIUM CHANNEL SUB-TYPES AND
;    TITLE OF INVENTION:  THEIR USE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SPRUNG HORN KRAMER & WOODS
;      STREET:  660 White Plains Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10591-5144
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MB
;      MEDIUM TYPE:  storage
;      COMPUTER:  NEC Powermate SX/20
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/456,200B
;      FILING DATE:  31-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/094,712
;      FILING DATE:  19-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/858,278
;      FILING DATE:  26-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,778
;      FILING DATE:  19-MAY-1993
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  DE 41 10 785
;      FILING DATE:  04-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kurt G. Briscoe
;      REGISTRATION NUMBER:  33,141
;      REFERENCE/DOCKET NUMBER:  Bayer 8398.3-KGB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 332-1700
;      TELEFAX:  (914) 332-1844
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6232 nucleotides
;      TYPE:  Nucleotide
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA
US-08-456-200B-11

  Query Match             93.3%;  Score 14;  DB 4;  Length 6232;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCTGCTGAGG 15
           ||||||||||||||
Db     770 TCCGCCTGCTGAGG 783


RESULT 7
US-08-455-543A-8
; Sequence 8, Application US/08455543A
; Patent No. 5792846
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/455,543A
;      FILING DATE:  May 31, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/223,305
;      FILING DATE:  April 4, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/868,354
;      FILING DATE:  April 10, 1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/745,206
;      FILING DATE:  15-AUG-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/620,250
;      FILING DATE:  30-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/482,384
;      FILING DATE:  20-FEB-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/603,751
;      FILING DATE:  04-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US89/01408
;      FILING DATE:  04-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/176,899
;      FILING DATE:  04-APR-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-52517
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  144..6857
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..143
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  6855..7175
US-08-455-543A-8

  Query Match             93.3%;  Score 14;  DB 1;  Length 7175;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCTGCTGAGG 15
           ||||||||||||||
Db    1882 TCCGCCTGCTGAGG 1895


RESULT 8
US-08-193-078B-8
; Sequence 8, Application US/08193078B
; Patent No. 5846757
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWN, MARTIN, HALLER & McCLAIN
;      STREET:  1660 UNION STREET
;      CITY:  SAN DIEGO
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/193,078B
;      FILING DATE:  07-FEB-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  US 07/868,354
;      FILING DATE:  10-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/745,206
;      FILING DATE:  15-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-53607
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-238-0999
;      TELEFAX:  619-238-0062
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  144..6857
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..143
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  6855..7175
US-08-193-078B-8

  Query Match             93.3%;  Score 14;  DB 2;  Length 7175;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCTGCTGAGG 15
           ||||||||||||||
Db    1882 TCCGCCTGCTGAGG 1895


RESULT 9
US-08-223-305C-8
; Sequence 8, Application US/08223305C
; Patent No. 5851824
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/223,305C
;      FILING DATE:  April 4, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/868,354
;      FILING DATE:  April 10, 1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/745,206
;      FILING DATE:  15-AUG-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/620,250
;      FILING DATE:  30-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/482,384
;      FILING DATE:  20-FEB-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/603,751
;      FILING DATE:  04-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US89/01408
;      FILING DATE:  04-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/176,899
;      FILING DATE:  04-APR-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  52516  (P519739)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  144..6857
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..143
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  6855..7175
US-08-223-305C-8

  Query Match             93.3%;  Score 14;  DB 2;  Length 7175;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCTGCTGAGG 15
           ||||||||||||||
Db    1882 TCCGCCTGCTGAGG 1895


RESULT 10
US-08-149-097D-8
; Sequence 8, Application US/08149097D
; Patent No. 5874236
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/149,097D
;       FILING DATE:  05-NOV-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/105,536
;       FILING DATE:  11-AUG-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/US92/06903
;       FILING DATE:  14-AUG-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/914,231
;       FILING DATE:  13-JUL-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/868,354
;       FILING DATE:  10-APR-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/745,206
;       FILING DATE:  15-AUG-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/620,250
;       FILING DATE:  30-NOV-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/482,384
;       FILING DATE:  20-FEB-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/603,751
;       FILING DATE:  04-APR-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/US89/01408
;       FILING DATE:  04-APR-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/176,899
;       FILING DATE:  04-APR-1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Seidman, Stephanie L.
;       REGISTRATION NUMBER:  33,779
;       REFERENCE/DOCKET NUMBER:  6362-55038
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 238-0999
;       TELEFAX:  (619) 238-0062
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7175 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  144..6857
;     FEATURE:
;       NAME/KEY:  5'UTR
;       LOCATION:  1..143
;     FEATURE:
;       NAME/KEY:  3'UTR
;       LOCATION:  6855..7175
US-08-149-097D-8

  Query Match             93.3%;  Score 14;  DB 2;  Length 7175;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCGCCTGCTGAGG 15
          ||||||||||||||
Db   1882 TCCGCCTGCTGAGG 1895


RESULT 11
US-08-949-386-8
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; Sequence 8, Application US/08949386
; Patent No. 6090623
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Gillespie, Alison
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/949,386
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/290,012
;      FILING DATE:  11-AUG-1994
;      APPLICATION NUMBER:  08/149,097
;      FILING DATE:  5-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/105,536
;      FILING DATE:  11-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  519808
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 238-0999
;      TELEFAX:  (619) 238-0062
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  144..6857
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..143
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  6855..7175
US-08-949-386-8

  Query Match             93.3%;  Score 14;  DB 3;  Length 7175;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCGCCTGCTGAGG 15
          ||||||||||||||
Db   1882 TCCGCCTGCTGAGG 1895


RESULT 12
US-08-450-562-
; Sequence 8,  plication US/08450562
; Patent No. 6096514
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;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Gillespie, Alison
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,562
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/404,950
;      FILING DATE:  13-MAR-1995
;      APPLICATION NUMBER:  08/336,257
;      FILING DATE:  7-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/314,083
;      FILING DATE:  28-SEPT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/311,363
;      FILING DATE:  23-SEPT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/290,012
;      FILING DATE:  11-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/223,305
;      FILING DATE:  4-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/193,078
;      FILING DATE:  07-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/149,097
;      FILING DATE:  5-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/105,536
;      FILING DATE:  11-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/914,231
;      FILING DATE:  13-JULY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/868,354
;      FILING DATE:  10-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/06903
;      FILING DATE:  14-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/745,206
;      FILING DATE:  15-AUG-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/620,250
;      FILING DATE:  30-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/603,751
;      FILING DATE:  08-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/482,384
;      FILING DATE:  02-FEB-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US89/01408
;      FILING DATE:  04-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/176,899
;      FILING DATE:  04-APR-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-519812
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 238-0999
;      TELEFAX:  (619) 238-0062
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  144..6857
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..143
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  6855..7175
US-08-450-562-8

  Query Match             93.3%;  Score 14;  DB 3;  Length 7175;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TC  CTGCTGAGG 15
           !!!!!!!!!!!!!!
Db    1882 TCCGCCTGCTGAGG 1895


RESULT 13
US-08-984-709A-8
; Sequence 8, Application US/08984709A
; Patent No. 6320032
;  GENERAL INFORMATION:
;    APPLICANT:  Williams, Mark E.
;    APPLICANT:  Stauderman, Kenneth A.
;    APPLICANT:  Harpold, Michael M.
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Heller Ehrman White & McAuliffe
;      STREET:  4250 Executive Square, Suite 700
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/984,709A
;      FILING DATE:  02-DEC-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  24735-9815 (formerly 6362-9815)
;    TELECOMMUNICATION INFORMATION:
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;       TELEPHONE:  (619) 450-8400
;       TELEFAX:  (619) 587-5360
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7175 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  144..6857
;     FEATURE:
;       NAME/KEY:  5'UTR
;       LOCATION:  1..143
;     FEATURE:
;       NAME/KEY:  3'UTR
;       LOCATION:  6855..7175
US-08-984-709A-8

  Query Match             93.3%;  Score 14;  DB 4;  Length 7175;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCTGCTGAGG 15
           ||||||||||||||
Db    1882 TCCGCCTGCTGAGG 1895


RESULT 14
US-09-268-163-7
; Sequence 7, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
;  APPLICANT: Lipscombe, Diane
;  APPLICANT: Schorge, Stephanie
;  TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
;  FILE REFERENCE: B1055/7000
;  CURRENT APPLICATION NUMBER: US/09/268,163B
;  CURRENT FILING DATE: 1999-03-12
;  EARLIER APPLICATION NUMBER: US 60/077,901
;  EARLIER FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 7177
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 146..6856
US-09-268-163-7

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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCTGCTGAGG 15
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Db    1884 TCCGCCTGCTGAGG 1897


RESULT 15
US-08-713-118-1
; Sequence 1, Application US/08713118
; Patent No. 6040436
;  GENERAL INFORMATION:
;    APPLICANT:  Franco, Rodrigo
;    APPLICANT:  Sun Chen, Ai Ru
;    APPLICANT:  Suey, David J.
;    TITLE OF INVENTION:  NUCLEIC ACID ENCODING HUMAN NEURONAL
;    TITLE OF INVENTION:  CALCIUM CHANNEL SUBUNITS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173-4799
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/713,118
;      FILING DATE:  16-SEP-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mata, Elizabeth W.
;      REGISTRATION NUMBER:  38,236
;      REFERENCE/DOCKET NUMBER:  ACC96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7266 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  92..7102
US-08-713-118-1

  Query Match             93.3%;  Score 14;  DB 3;  Length 7266;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCTGCTGAGG 15
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Job time : 16.9091 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 16:08:01 ; Search time 539.591 Seconds
(without alignments)
375.200 Million cell updates/sec

Title: US-09-856-803-6
Perfect score: 15
Sequence: 1 gtccgcctgctgagg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
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7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	5	15	100.0	683	10	BG284879	BG284879 602409113
	6	15	100.0	701	12	CNS04KMI	AL295011 Tetraodon
	7	15	100.0	848	10	BI767868	BI767868 603060993
	8	15	100.0	853	10	BI915042	BI915042 603177231
	9	15	100.0	950	9	AL553611	AL553611 AL553611
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	11	14	93.3	179	9	AA015272	AA015272 mh30g12.r
	12	14	93.3	240	10	BE419553	BE419553 WWS014.E1
	13	14	93.3	279	10	BE770021	BE770021 CM1-FT005
c	14	14	93.3	395	9	AA763693	AA763693 vp06a08.r
c	15	14	93.3	404	9	AI210517	AI210517 i7g01a1.r
	16	14	93.3	501	10	BG366430	BG366430 HVSMEi000
c	17	14	93.3	503	10	BM309817	BM309817 D2C13 Die
c	18	14	93.3	505	9	AV643146	AV643146 AV643146
	19	14	93.3	511	10	BF478400	BF478400 WHE2001_G
c	20	14	93.3	519	12	TA326F10P	AL492725 T. brucei
	21	14	93.3	529	10	BE499548	BE499548 WHE0961_B
	22	14	93.3	531	12	TA326F10Q	AL491062 T. brucei
	23	14	93.3	544	6	BI140168	BI140168 IP1_50_A0
c	24	14	93.3	577	10	BF891826	BF891826 IL0-MT013
	25	14	93.3	584	9	AU241418	AU241418 AU241418
c	26	14	93.3	595	9	AW288744	AW288744 707003F05
	27	14	93.3	610	12	AQ659341	AQ659341 Sheared D
	28	14	93.3	616	12	AQ650898	AQ650898 Sheared D
c	29	14	93.3	623	9	AA803093	AA803093 GM06974.5
	30	14	93.3	630	9	AU179691	AU179691 AU179691
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c	34	14	93.3	651	10	BM316850	BM316850 fw79b06.x
c	35	14	93.3	687	9	AV611157	AV611157 AV611157
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	37	14	93.3	701	10	BG856218	BG856218 1024045A0
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	39	14	93.3	875	12	CNS02LO1	AL203050 Tetraodon
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	41	14	93.3	892	10	BG714019	BG714019 602674429
c	42	14	93.3	893	12	CNS031KQ	AL223667 Tetraodon
c	43	14	93.3	934	12	CNS01GLJ	AL143288 Anopheles
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ALIGNMENTS

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DEFINITION AV647785 GLC Homo sapiens cDNA clone GLCBCA03 3', mRNA sequence.
ACCESSION AV647785
VERSION AV647785.1 GI:9868799
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 427)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES Location/Qualifiers
source 1. .427
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCBCA03"
/clone_lib="GLC"
/tissue_type="corresponding non cancerous liver tissue"
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/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

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Db    143 GTCCGCCTGCTGAGG 157


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LOCUS       AQ759327                580 bp    DNA     linear   GSS 27-JUL-1999
DEFINITION  HS_3116_A1_A03_T7C CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3116 Col=5 Row=A, DNA sequence.
ACCESSION   AQ759327
VERSION     AQ759327.1  GI:5624640
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 580)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server: http://www.htsc.washington.edu
            Plate: 3116  row: A  column: 5
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 580.
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ORIGIN

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCTGCTGAGG 15
          |||||||||||||||
Db    577 GTCCGCCTGCTGAGG 563


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BI907636
LOCUS       BI907636                659 bp    mRNA    linear   EST 16-OCT-2001
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            mRNA sequence.
ACCESSION   BI907636
VERSION     BI907636.1  GI:16170473
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 659)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11539  row: i  column: 11
            High quality sequence stop: 655.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
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                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
BASE COUNT      127 a    198 c    194 g    140 t
ORIGIN

  Query Match            100.0%;  Score 15;  DB 10;  Length 659;
  Best Local Similarity  100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCTGCTGAGG 15
          |||||||||||||||
Db    125 GTCCGCCTGCTGAGG 139


RESULT 4
BJ001358/c
LOCUS       BJ001358                671 bp    mRNA    linear   EST 05-DEC-2001
DEFINITION  BJ001358 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA006C12 5',
            mRNA sequence.
ACCESSION   BJ001358
VERSION     BJ001358.1  GI:17361625
KEYWORDS    EST.
SOURCE      Japanese medaka.
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1  (bases 1 to 671)
  AUTHORS   Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
  TITLE     Medaka EST Project in Takeda's lab
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
```

```
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .671
                     /organism="Oryzias latipes"
                     /strain="Hd-rR"
                     /db_xref="taxon:8090"
                     /clone="MF01SSA006C12"
                     /clone_lib="MF01SSA cDNA"
                     /sex="mixture of female and male"
                     /tissue_type="whole embryo"
                     /dev_stage="segmentation stage 20 - 25"
BASE COUNT      152 a    149 c    197 g    173 t
ORIGIN

  Query Match             100.0%;  Score 15;  DB 10;  Length 671;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCTGCTGAGG 15
           |||||||||||||||
Db     386 GTCCGCCTGCTGAGG 372


RESULT 5
BG284879
LOCUS       BG284879                683 bp    mRNA    linear   EST 21-FEB-2001
DEFINITION  602409113F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4538187 5',
            mRNA sequence.
ACCESSION   BG284879
VERSION     BG284879.1  GI:13036277
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 683)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10464  row: i  column: 04
            High quality sequence stop: 678.
FEATURES             Location/Qualifiers
     source          1. .683
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4538187"
                     /clone_lib="NIH_MGC_91"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.4 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      127 a    203 c    209 g    144 t
ORIGIN

  Query Match             100.0%;  Score 15;  DB 10;  Length 683;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCTGCTGAGG 15
           |||||||||||||||
Db     165 GTCCGCCTGCTGAGG 179


RESULT 6
CNS04KMI
LOCUS       CNS04KMI                701 bp    DNA     linear   GSS 21-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            116D24 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL295011
VERSION     AL295011.1  GI:8033591
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 701)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 701)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 701)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .701
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="116D24"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG116DB12SP1~end :
                     PUC-Ori"
BASE COUNT      137 a    190 c    169 g    197 t      8 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 12;  Length 701;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCTGCTGAGG 15
           |||||||||||||||
Db      42 GTCCGCCTGCTGAGG 56


RESULT 7
BI767868
LOCUS       BI767868                848 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603060993F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5210231 5',
            mRNA sequence.
ACCESSION   BI767868
VERSION     BI767868.1  GI:15759446
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
```

```
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11527  row: j  column: 24
            High quality sequence stop: 845.
FEATURES             Location/Qualifiers
     source          1. .848
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5210231"
                     /clone_lib="NIH_MGC_122"
                     /lab_host="DH10B"
                     /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
                     anonymous pool of 24 week female lung, 16 week female
                     spleen, and 20-22 week male spleens.  Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon  cloning).  Average insert size 1.4 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was  constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking  code 026. Note:
                     this is a NIH_MGC Library."
BASE COUNT      157 a    265 c    230 g    195 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 10;  Length 848;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCTGCTGAGG 15
           |||||||||||||||
Db     148 GTCCGCCTGCTGAGG 162


RESULT 8
BI915042
LOCUS       BI915042                853 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603177231F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5241774 5',
            mRNA sequence.
ACCESSION   BI915042
VERSION     BI915042.1  GI:16179135
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11609  row: m  column: 07
            High quality sequence stop: 840.
FEATURES             Location/Qualifiers
     source          1. .853
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5241774"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      161 a    269 c    229 g    194 t
ORIGIN

  Query Match             100.0%;  Score 15;  DB 10;  Length 853;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCTGCTGAGG 15
           |||||||||||||||
Db     136 GTCCGCCTGCTGAGG 150


RESULT 9
AL553611
LOCUS       AL553611                950 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL553611 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI078YB15 5
            prime, mRNA sequence.
ACCESSION   AL553611
VERSION     AL553611.1  GI:12893606
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 950)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .950
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DI078YB15"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      183 a    291 c    262 g    210 t      4 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 9;  Length 950;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCTGCTGAGG 15
           |||||||||||||||
Db     123 GTCCGCCTGCTGAGG 137
```

RESULT 10
CNS041TO/c
LOCUS CNS041TO 1013 bp DNA linear GSS 18-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 075K01 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL270645
VERSION AL270645.1 GI:7992574
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 1013)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1013)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1013)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES Location/Qualifiers
source 1. .1013
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="075K01"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG075AF01LP1~end : T7"
BASE COUNT 291 a 227 c 280 g 214 t 1 others
ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 1013;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCTGCTGAGG 15
||||||||||||||||
Db 42 GTCCGCCTGCTGAGG 28

RESULT 11
AA015272
LOCUS AA015272 179 bp mRNA linear EST 21-JAN-1997
DEFINITION mh30g12.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone IMAGE:444070 5' similar to gb:X16706 FOS-RELATED ANTIGEN 2 (HUMAN);, mRNA sequence.
ACCESSION AA015272
VERSION AA015272.1 GI:1476304
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 179)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:269406
Trace considered overall poor quality
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .179
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:444070"
/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 33 a 55 c 44 g 47 t
ORIGIN

Query Match 93.3%; Score 14; DB 9; Length 179;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCCGCCTGCTGAGG 15
||||||||||||||
Db 88 TCCGCCTGCTGAGG 101

RESULT 12
BE419553
LOCUS BE419553 240 bp mRNA linear EST 24-JUL-2000
DEFINITION WWS014.E1R000101 ITEC WWS Wheat Scutellum Library Triticum aestivum cDNA clone WWS014.E1, mRNA sequence.
ACCESSION BE419553
VERSION BE419553.1 GI:9417399
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 240)
AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier ,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
TITLE International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae

```
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Schuch W
            Zeneca Wheat Improvement Centre, Norwich Research Park
            Colney Lane, Norwich NR4 7UH UNITED KINGDOM
            Tel: 44 1603 250 2600
            Fax: 44 1603 250 699
            Email: wolfgang.schuch@aguk.zeneca.com
            International Triticeae EST Cooperative (ITEC)
            http://wheat.pw.usda.gov/genome.
FEATURES             Location/Qualifiers
     source          1. .240
                     /organism="Triticum aestivum"
                     /cultivar="Novosibirskaya 67"
                     /db_xref="taxon:4565"
                     /clone="WWS014.E1"
                     /clone_lib="ITEC WWS Wheat Scutellum Library"
                     /tissue_type="scutellum callus"
                     /note="M13 Reverse sequencing primer used for 5' end of
                     clone. "
BASE COUNT       17 a    117 c     62 g     44 t
ORIGIN

  Query Match             93.3%;  Score 14;  DB 10;  Length 240;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCTGCTGAGG 15
           ||||||||||||||
Db      25 TCCGCCTGCTGAGG 38


RESULT 13
BE770021
LOCUS       BE770021                279 bp    mRNA    linear   EST 20-SEP-2000
DEFINITION  CM1-FT0051-200600-281-h11 FT0051 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE770021
VERSION     BE770021.1  GI:10223679
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 279)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM1-FT0051-200
            600-281-h11&t3=2000-06-20&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 19
            High quality sequence stop: 279.
FEATURES             Location/Qualifiers
     source          1. .279
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="FT0051"
                     /dev_stage="Adult"
                     /note="Organ: prostate_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       73 a     62 c     52 g     92 t
ORIGIN

  Query Match             93.3%;  Score 14;  DB 10;  Length 279;
  Best Local Similarity   100.0%;  Pred. No. 7e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TCCGCCTGCTGAGG 15
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Db      85 TCCGCCTGCTGAGG 98


RESULT 14
AA763693/c
LOCUS       AA763693                395 bp    mRNA    linear   EST 27-JAN-1998
DEFINITION  vp06a08.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
            IMAGE:1067798 5', mRNA sequence.
ACCESSION   AA763693
VERSION     AA763693.1  GI:2813775
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 395)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:590158
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 329.
FEATURES             Location/Qualifiers
     source          1. .395
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1067798"
                     /clone_lib="Soares_mammary_gland_NbMMG"
                     /sex="male"
                     /tissue_type="mammary gland"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
                     ) with a modified polylinker; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                     constructed and normalized by Bento Soares and M.Fatima
```

Bonaldo."
BASE COUNT 82 a 117 c 91 g 105 t
ORIGIN

Query Match 93.3%; Score 14; DB 9; Length 395;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCTGCTGAG 14
||||||||||||||
Db 346 GTCCGCCTGCTGAG 333

RESULT 15
AI210517/c
LOCUS AI210517 404 bp mRNA linear EST 19-OCT-1998
DEFINITION i7g01a1.r1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone i7g01a1 5', mRNA sequence.
ACCESSION AI210517
VERSION AI210517.1 GI:3772459
KEYWORDS EST.
SOURCE Emericella nidulans.
ORGANISM Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
REFERENCE 1 (bases 1 to 404)
AUTHORS Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe,B.
TITLE An Aspergillus nidulans EST Database
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: i7g01a1.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
Seq primer: T3
High quality sequence stop: 386.
FEATURES Location/Qualifiers
source 1. .404
/organism="Emericella nidulans"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="i7g01a1"
/clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 102 a 114 c 118 g 61 t 9 others
ORIGIN

Query Match 93.3%; Score 14; DB 9; Length 404;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCTGCTGAG 14
||||||||||||||
Db 146 GTCCGCCTGCTGAG 133

Search completed: November 2, 2002, 17:57:10
Job time : 544.591 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 14:22:04 ; Search time 18.5455 Seconds
(without alignments)
264.899 Million cell updates/sec

Title: US-09-856-803-7
Perfect score: 20
Sequence: 1 ccccgccgtgggtccgcccg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	230	4	US-09-437-457-8	Sequence 8, Appli
c 2		15.8	79.0	1730	6	5223391-8	Patent No. 5223391
c 3		15.2	76.0	40	2	US-08-778-494B-91	Sequence 91, Appl
c 4		15.2	76.0	40	2	US-08-778-494B-92	Sequence 92, Appl
c 5		15.2	76.0	40	2	US-08-778-494B-104	Sequence 104, App
c 6		15.2	76.0	41	2	US-08-778-494B-97	Sequence 97, Appl
c 7		15.2	76.0	830	3	US-09-165-240-1	Sequence 1, Appli
c 8		15.2	76.0	830	4	US-09-568-059-1	Sequence 1, Appli
c 9		15.2	76.0	833	3	US-09-165-240-2	Sequence 2, Appli
c 10		15.2	76.0	833	4	US-09-568-059-2	Sequence 2, Appli
11		15.2	76.0	837	2	US-08-658-665-72	Sequence 72, Appl
12		15.2	76.0	837	4	US-08-796-101-36	Sequence 36, Appl
13		15.2	76.0	837	4	US-09-085-273-72	Sequence 72, Appl
14		15.2	76.0	961	1	US-07-921-807B-9	Sequence 9, Appli
15		15.2	76.0	961	1	US-08-441-944A-9	Sequence 9, Appli
c 16		15.2	76.0	2253	6	5457037-2	Patent No. 5457037
c 17		15.2	76.0	2394	4	US-08-797-358B-1	Sequence 1, Appli
c 18		15.2	76.0	2625	6	5457037-4	Patent No. 5457037
c 19		15.2	76.0	3336	6	5457037-1	Patent No. 5457037
20		15.2	76.0	3962	2	US-08-658-665-189	Sequence 189, App
21		15.2	76.0	5062	2	US-08-658-665-187	Sequence 187, App
22		15.2	76.0	5062	4	US-08-796-101-42	Sequence 42, Appl
23		15.2	76.0	5234	2	US-08-658-665-73	Sequence 73, Appl
24		15.2	76.0	5234	4	US-08-796-101-37	Sequence 37, Appl
25		15.2	76.0	5234	4	US-09-085-273-73	Sequence 73, Appl
26		15.2	76.0	5302	2	US-08-658-665-190	Sequence 190, App
27		15.2	76.0	5302	4	US-08-796-101-40	Sequence 40, Appl
28		15.2	76.0	5434	2	US-08-841-349-1	Sequence 1, Appli
c 29		15.2	76.0	71989	4	US-09-443-501A-2	Sequence 2, Appli
c 30		15.2	76.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
c 31		14.4	72.0	1873	4	US-09-011-540-1	Sequence 1, Appli
32		14.4	72.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
33		14.4	72.0	4411529	4	US-09-103-840A-1	Sequence 1, Appli
34		14.2	71.0	168	1	US-08-488-144-24	Sequence 24, Appl
c 35		14.2	71.0	188	4	US-09-257-541-4	Sequence 4, Appli
c 36		14.2	71.0	480	5	PCT-US95-08295-18	Sequence 18, Appl
37		14.2	71.0	642	3	US-08-911-853-12	Sequence 12, Appl
38		14.2	71.0	642	4	US-09-479-409-12	Sequence 12, Appl
39		14.2	71.0	642	4	US-09-479-453-12	Sequence 12, Appl
c 40		14.2	71.0	849	3	US-08-807-300-2	Sequence 2, Appli
41		14.2	71.0	850	4	US-08-998-416-314	Sequence 314, App
42		14.2	71.0	1247	1	US-08-278-729A-32	Sequence 32, Appl
43		14.2	71.0	1247	1	US-08-155-343A-32	Sequence 32, Appl
44		14.2	71.0	1247	1	US-08-406-672-32	Sequence 32, Appl
45		14.2	71.0	1247	1	US-08-643-563A-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-437-457-8
; Sequence 8, Application US/09437457
; Patent No. 6273893
; GENERAL INFORMATION:
; APPLICANT: Giordano, Anthony
; APPLICANT: Xavier, Ashish
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
; TITLE OF INVENTION: INTERACTIONS AND MRNA FUNCTIONALITY
; FILE REFERENCE: 50093/014001
; CURRENT APPLICATION NUMBER: US/09/437,457
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-437-457-8

Query Match 100.0%; Score 20; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCCG 20
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Db 155 CCCCGCCGTGGGTCCGCCCG 174

RESULT 2
5223391-8/c
;Patent No. 5223391
; APPLICANT: COEN, DONALD M.;DIGARD, PAUL E.
; TITLE OF INVENTION: INHIBITIORS OF HERPES SIMPLEX VIRUS
;REPLICATION
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,634
; FILING DATE: 21-FEB-1990
;SEQ ID NO:8:
; LENGTH: 1730
5223391-8

Query Match 79.0%; Score 15.8; DB 6; Length 1730;
Best Local Similarity 89.5%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCC 19
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Db     464 CGCCGCCGTGGGTCCGCGC 446


RESULT 3
US-08-778-494B-91/c
; Sequence 91, Application US/08778494B
; Patent No. 5962272
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Zhu, York
;    APPLICANT:  Diachenko, Luda
;    APPLICANT:  Siebert, Paul
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR FULL-LENGTH cDNA
;    TITLE OF INVENTION:  CLONING
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Saliwanchik, Lloyd & Saliwanchik
;      STREET:  2421 N.W. 41st Street, Suite A-1
;      CITY:  Gainesville
;      STATE:  Florida
;      COUNTRY:  USA
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/778,494B
;      FILING DATE:  03-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/582,562
;      FILING DATE:  03-JAN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pace, Doran R.
;      REGISTRATION NUMBER:  38,261
;      REFERENCE/DOCKET NUMBER:  CL-7C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (352) 375-8100
;      TELEFAX:  (352) 372-5800
;  INFORMATION FOR SEQ ID NO:  91:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (synthetic)
US-08-778-494B-91

  Query Match             76.0%;  Score 15.2;  DB 2;  Length 40;
  Best Local Similarity   85.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCCG 20
           |||||||||| | |||| ||
Db      40 CCCCGCCGTGCGGCCGCTCG 21


RESULT 4
US-08-778-494B-92/c
; Sequence 92, Application US/08778494B
; Patent No. 5962272
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Zhu, York
;    APPLICANT:  Diachenko, Luda
;    APPLICANT:  Siebert, Paul
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR FULL-LENGTH cDNA
;    TITLE OF INVENTION:  CLONING
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Saliwanchik, Lloyd & Saliwanchik
;      STREET:  2421 N.W. 41st Street, Suite A-1
;      CITY:  Gainesville
;      STATE:  Florida
;      COUNTRY:  USA
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/778,494B
;      FILING DATE:  03-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/582,562
;      FILING DATE:  03-JAN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pace, Doran R.
;      REGISTRATION NUMBER:  38,261
;      REFERENCE/DOCKET NUMBER:  CL-7C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (352) 375-8100
;      TELEFAX:  (352) 372-5800
;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (synthetic)
US-08-778-494B-92

  Query Match             76.0%;  Score 15.2;  DB 2;  Length 40;
  Best Local Similarity   85.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCCG 20
           |||||||||| | |||| ||
Db      40 CCCCGCCGTGCGGCCGCTCG 21


RESULT 5
US-08-778-494B-104/c
; Sequence 104, Application US/08778494B
; Patent No. 5962272
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Zhu, York
;    APPLICANT:  Diachenko, Luda
;    APPLICANT:  Siebert, Paul
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR FULL-LENGTH cDNA
;    TITLE OF INVENTION:  CLONING
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Saliwanchik, Lloyd & Saliwanchik
;      STREET:  2421 N.W. 41st Street, Suite A-1
;      CITY:  Gainesville
;      STATE:  Florida
;      COUNTRY:  USA
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/778,494B
;      FILING DATE:  03-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/582,562
;      FILING DATE:  03-JAN-1996
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```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pace, Doran R.
;      REGISTRATION NUMBER:  38,261
;      REFERENCE/DOCKET NUMBER:  CL-7C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (352) 375-8100
;      TELEFAX:  (352) 372-5800
;  INFORMATION FOR SEQ ID NO:  104:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (synthetic)
US-08-778-494B-104

  Query Match            76.0%;  Score 15.2;  DB 2;  Length 40;
  Best Local Similarity  85.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||  | |||| ||
Db     40 CCCCGCCGTGCGGCCGCTCG 21


RESULT 6
US-08-778-494B-97/c
; Sequence 97, Application US/08778494B
; Patent No. 5962272
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Zhu, York
;    APPLICANT:  Diachenko, Luda
;    APPLICANT:  Siebert, Paul
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR FULL-LENGTH cDNA
;    TITLE OF INVENTION:  CLONING
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Saliwanchik, Lloyd & Saliwanchik
;      STREET:  2421 N.W. 41st Street, Suite A-1
;      CITY:  Gainesville
;      STATE:  Florida
;      COUNTRY:  USA
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/778,494B
;      FILING DATE:  03-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/582,562
;      FILING DATE:  03-JAN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pace, Doran R.
;      REGISTRATION NUMBER:  38,261
;      REFERENCE/DOCKET NUMBER:  CL-7C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (352) 375-8100
;      TELEFAX:  (352) 372-5800
;  INFORMATION FOR SEQ ID NO:  97:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (synthetic)
US-08-778-494B-97

  Query Match            76.0%;  Score 15.2;  DB 2;  Length 41;
  Best Local Similarity  85.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||  | |||| ||
Db     41 CCCCGCCGTGCGGCCGCTCG 22


RESULT 7
US-09-165-240-1/c
; Sequence 1, Application US/09165240A
; Patent No. 6087164
; GENERAL INFORMATION:
;  APPLICANT: Hochberg, Abraham
;  APPLICANT: Ayesh, Suhail
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
;  TITLE OF INVENTION: TUMOR-SPECIFIC CYTOTOXICITY
;  FILE REFERENCE: 9457-0014-999
;  CURRENT APPLICATION NUMBER: US/09/165,240A
;  CURRENT FILING DATE: 1998-10-01
;  EARLIER APPLICATION NUMBER: US 08/943,608
;  EARLIER FILING DATE: 1997-10-03
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 830
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-165-240-1

  Query Match            76.0%;  Score 15.2;  DB 3;  Length 830;
  Best Local Similarity  85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||  |||||||||  | |
Db     62 CCCCGCTGTGGGTCCGTCGG 43


RESULT 8
US-09-568-059-1/c
; Sequence 1, Application US/09568059
; Patent No. 6306833
; GENERAL INFORMATION:
;  APPLICANT:  Hochberg, Abraham
;  APPLICANT:  Ayesh, Suhail
;  TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR INDUCING
;  TITLE OF INVENTION:  TUMOR-SPECIFIC CYTOTOXICITY
;  FILE REFERENCE:  9457-0014-999
;  CURRENT APPLICATION NUMBER: US/09/568,059
;  CURRENT FILING DATE:  2000-05-10
;  PRIOR APPLICATION NUMBER:  09/165,240
;  PRIOR FILING DATE:  1998-10-01
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 830
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-568-059-1

  Query Match            76.0%;  Score 15.2;  DB 4;  Length 830;
  Best Local Similarity  85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
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Db     62 CCCCGCTGTGGGTCCGTCGG 43


RESULT 9
US-09-165-240-2/c
; Sequence 2, Application US/09165240A
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; Patent No. 6087164
; GENERAL INFORMATION:
;  APPLICANT: Hochberg, Abraham
;  APPLICANT: Ayesh, Suhail
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
;  TITLE OF INVENTION: TUMOR-SPECIFIC CYTOTOXICITY
;  FILE REFERENCE: 9457-0014-999
;  CURRENT APPLICATION NUMBER: US/09/165,240A
;  CURRENT FILING DATE: 1998-10-01
;  EARLIER APPLICATION NUMBER: US 08/943,608
;  EARLIER FILING DATE: 1997-10-03
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 833
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-165-240-2

  Query Match             76.0%;  Score 15.2;  DB 3;  Length 833;
  Best Local Similarity   85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||| ||||||||| | |
Db     50 CCCCGCTGTGGGTCCGTCGG 31


RESULT 10
US-09-568-059-2/c
; Sequence 2, Application US/09568059
; Patent No. 6306833
; GENERAL INFORMATION:
;  APPLICANT:  Hochberg, Abraham
;  APPLICANT:  Ayesh, Suhail
;  TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR INDUCING
;  TITLE OF INVENTION:  TUMOR-SPECIFIC CYTOTOXICITY
;  FILE REFERENCE:  9457-0014-999
;  CURRENT APPLICATION NUMBER: US/09/568,059
;  CURRENT FILING DATE:  2000-05-10
;  PRIOR APPLICATION NUMBER:   09/165,240
;  PRIOR FILING DATE:   1998-10-01
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 833
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-568-059-2

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 833;
  Best Local Similarity   85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||| ||||||||| | |
Db     50 CCCCGCTGTGGGTCCGTCGG 31


RESULT 11
US-08-658-665-72
; Sequence 72, Application US/08658665
; Patent No. 5997878
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Pincus, Steven E.
;    APPLICANT:  Cox, William I.
;    APPLICANT:  Kauffman, Elizabeth K.
;    TITLE OF INVENTION:  Recombinant Poxvirus - Cytomegalovirus,
;    TITLE OF INVENTION:  Compositions and Uses
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/658,665
;      FILING DATE:  05-JUN-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer Esq., William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2720.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)840-3333
;      TELEFAX:  (212)840-0712
;  INFORMATION FOR SEQ ID NO:  72:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  837 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-658-665-72

  Query Match             76.0%;  Score 15.2;  DB 2;  Length 837;
  Best Local Similarity   85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          || ||||||| ||| |||||
Db    609 CCGCGCCGTGCGTCTGCCCG 628


RESULT 12
US-08-796-101-36
; Sequence 36, Application US/08796101
; Patent No. 6183752
;  GENERAL INFORMATION:
;    APPLICANT:  EPSTEIN, STEPHEN E.
;    APPLICANT:  FINKEL, TOREN
;    APPLICANT:  SPEIR, EDITH
;    APPLICANT:  ZHOU, YI FU
;    APPLICANT:  ZHU, JIANHUI
;    APPLICANT:  ERDILE, LORNE
;    APPLICANT:  PINCUS, STEVEN
;    TITLE OF INVENTION:  RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,
;    TITLE OF INVENTION:  PROPHYLAXIS AND THERAPY
;    NUMBER OF SEQUENCES:  184
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CURTIS, MORRIS & SAFFORD, P.C.
;      STREET:  530 FIFTH AVENUE
;      CITY:  NEW YORK
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/796,101
;      FILING DATE:  05-FEB-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KOWALSKI, THOMAS J.
;      REGISTRATION NUMBER:  32,147
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 764-5574
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  837 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-796-101-36

  Query Match            76.0%;  Score 15.2;  DB 4;  Length 837;
  Best Local Similarity  85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          || ||||||| ||| |||||
Db    609 CCGCGCCGTGCGTCTGCCCG 628


RESULT 13
US-09-085-273-72
; Sequence 72, Application US/09085273
; Patent No. 6267965
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Pincus, Steven E.
;    APPLICANT:  Cox, William I.
;    APPLICANT:  Kauffman, Elizabeth K.
;    TITLE OF INVENTION:  RECOMBINANT POXVIRUS - CYTOMEGALOVIRUS,
;    TITLE OF INVENTION:  COMPOSITIONS AND USES
;    NUMBER OF SEQUENCES:  176
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/085,273
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/471,014
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer Esq., William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2720
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  72:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  837 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-085-273-72

  Query Match            76.0%;  Score 15.2;  DB 4;  Length 837;
  Best Local Similarity  85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          || ||||||| ||| |||||
Db    609 CCGCGCCGTGCGTCTGCCCG 628


RESULT 14
US-07-921-807B-9
; Sequence 9, Application US/07921807B
; Patent No. 5474914
;  GENERAL INFORMATION:
;    APPLICANT:  SPAETE, RICHARD
;    TITLE OF INVENTION:  METHOD OF INCREASING EXPRESSION
;    TITLE OF INVENTION:  OF VIRAL PROTEINS
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION
;      STREET:  4560 Horton Street - R440
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/921,807B
;      FILING DATE:  29-SEP-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McCLUNG, BARBARA G.
;      REGISTRATION NUMBER:  33,113
;      REFERENCE/DOCKET NUMBER:  0209.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2708
;      TELEFAX:  (510) 655-3542
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  961 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-921-807B-9

  Query Match            76.0%;  Score 15.2;  DB 1;  Length 961;
  Best Local Similarity  85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          || ||||||| ||| |||||
Db    656 CCGCGCCGTGCGTCTGCCCG 675


RESULT 15
US-08-441-944A-9
; Sequence 9, Application US/08441944A
; Patent No. 5767250
;  GENERAL INFORMATION:
;    APPLICANT:  SPAETE, RICHARD
;    TITLE OF INVENTION:  METHOD OF INCREASING EXPRESSION
;    TITLE OF INVENTION:  OF VIRAL PROTEINS
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION
;      STREET:  4560 Horton Street - R440
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,944A
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/921,807
;      FILING DATE:  29-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McCLUNG, BARBARA G.
;      REGISTRATION NUMBER:  33,113
;      REFERENCE/DOCKET NUMBER:  0209.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2708
;      TELEFAX:  (510) 655-3542
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  961 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-441-944A-9

  Query Match             76.0%;  Score 15.2;  DB 1;  Length 961;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCCG 20
           || ||||||| ||| |||||
Db     656 CCGCGCCGTGCGTCTGCCCG 675


Search completed: November  2, 2002, 16:50:58
Job time : 22.5455 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 16:08:01 ; Search time 719.455 Seconds
(without alignments)
375.200 Million cell updates/sec

Title: US-09-856-803-7
Perfect score: 20
Sequence: 1 ccccgccgtgggtccgcccg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	406	10	BE245562	BE245562 TCBAP1E21
	2	20	100.0	646	10	BI911023	BI911023 603068746
c	3	19	95.0	1481	10	BM463935	BM463935 AGENCOURT
	4	18.4	92.0	427	9	AV647785	AV647785 AV647785
	5	18.4	92.0	659	10	BI907636	BI907636 603065545
	6	18.4	92.0	848	10	BI767868	BI767868 603060993
	7	18.4	92.0	853	10	BI915042	BI915042 603177231
	8	18.4	92.0	885	10	BI820274	BI820274 603036831
	9	18.4	92.0	950	9	AL553611	AL553611 AL553611
c	10	17.4	87.0	768	10	BG967364	BG967364 602833684
	11	17.4	87.0	788	10	BE619884	BE619884 601473140
c	12	17.4	87.0	917	10	BG687601	BG687601 602639211
c	13	17.4	87.0	973	10	BF338701	BF338701 602034396
c	14	17.4	87.0	1110	12	AG162212	AG162212 Pan trogl
c	15	16.8	84.0	245	9	AW447569	AW447569 89386 MAR
	16	16.8	84.0	417	9	BB679565	BB679565 BB679565
	17	16.8	84.0	477	9	AI393367	AI393367 tg44e06.x
	18	16.8	84.0	493	10	BE761414	BE761414 894098H07
c	19	16.8	84.0	498	12	CNS07F21	AL607915 Anopheles
c	20	16.8	84.0	640	10	BG435190	BG435190 602507710
c	21	16.8	84.0	647	10	BG719555	BG719555 602689916
c	22	16.8	84.0	656	9	AL537544	AL537544 AL537544
c	23	16.8	84.0	705	12	CNS01FQA	AL142163 Anopheles
c	24	16.8	84.0	755	10	BF673605	BF673605 602136015
c	25	16.8	84.0	778	12	CNS030N4	AL222457 Tetraodon
c	26	16.8	84.0	819	9	AL579466	AL579466 AL579466
	27	16.8	84.0	890	10	BE737269	BE737269 601305889
c	28	16.8	84.0	894	12	AG060214	AG060214 Pan trogl
	29	16.8	84.0	914	10	BF312798	BF312798 601896936
	30	16.8	84.0	919	10	BE959850	BE959850 601654770
c	31	16.8	84.0	928	10	BG282601	BG282601 602406267
	32	16.8	84.0	940	10	BE959115	BE959115 601645201
	33	16.8	84.0	960	10	BE974393	BE974393 601680376
c	34	16.8	84.0	1017	10	BG914353	BG914353 602810820
c	35	16.8	84.0	1025	12	AG055472	AG055472 Pan trogl
c	36	16.8	84.0	1048	12	AG082424	AG082424 Pan trogl
	37	16.8	84.0	1065	12	AG105184	AG105184 Pan trogl
c	38	16.8	84.0	1131	12	AG073901	AG073901 Pan trogl
c	39	16.8	84.0	1148	10	BG969355	BG969355 602836837
	40	16.8	84.0	1331	12	AG068186	AG068186 Pan trogl
	41	16.8	84.0	1687	12	AG072835	AG072835 Pan trogl
c	42	16.4	82.0	558	10	BG836814	BG836814 zm08_04h0
c	43	16.4	82.0	577	12	AQ660872	AQ660872 Sheared D
c	44	16.4	82.0	592	12	BH098657	BH098657 RPCI-24-3
c	45	16.4	82.0	758	12	AG080468	AG080468 Pan trogl

ALIGNMENTS

RESULT 1
BE245562
LOCUS BE245562 406 bp mRNA linear EST 03-OCT-2001
DEFINITION TCBAP1E2132 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2132, mRNA sequence.
ACCESSION BE245562
VERSION BE245562.1 GI:9097308
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 406)
AUTHORS Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
TITLE Pediatric Leukemia cDNA Sequencing Project
JOURNAL Unpublished (2000)
COMMENT Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@txccc.org
Citation: Carninci,P. and Hayashizaki,Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer.
FEATURES Location/Qualifiers
source 1. .406
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCBAP2132"
/clone_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"

/note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCCGCAGGAGGAG(T)VN 3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand was primed with a BamH1-dC primer [5'AGAGAGCTCGGATCCGCGGCCGCAATAATAATAAT(C) 3']. Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"

BASE COUNT 73 a 140 c 130 g 61 t 2 others
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 406;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCCG 20
||||||||||||||||||||
Db 158 CCCCGCCGTGGGTCCGCCCG 177

RESULT 2
BI911023
LOCUS BI911023 646 bp mRNA linear EST 16-OCT-2001
DEFINITION 603068746F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217922 5', mRNA sequence.
ACCESSION BI911023
VERSION BI911023.1 GI:16174544
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 646)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11547 row: k column: 11
High quality sequence stop: 643.

FEATURES Location/Qualifiers
source 1. .646
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5217922"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

BASE COUNT 114 a 209 c 189 g 134 t
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 646;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCCG 20
||||||||||||||||||||
Db 126 CCCCGCCGTGGGTCCGCCCG 145

RESULT 3
BM463935/c
LOCUS BM463935 1481 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6445415 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5539947 5', mRNA sequence.
ACCESSION BM463935
VERSION BM463935.1 GI:18512977
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1481)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12235 row: e column: 04
High quality sequence start: 88
High quality sequence stop: 451.

FEATURES Location/Qualifiers
source 1. .1481
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5539947"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 261 a 602 c 334 g 283 t 1 others
ORIGIN

Query Match 95.0%; Score 19; DB 10; Length 1481;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCGCCGTGGGTCCGCCCG 20
|||||||||||||||||||
Db 50 CCCGCCGTGGGTCCGCCCG 32

RESULT 4
AV647785
LOCUS AV647785 427 bp mRNA linear EST 15-JAN-2002
DEFINITION AV647785 GLC Homo sapiens cDNA clone GLCBCA03 3', mRNA sequence.
ACCESSION AV647785
VERSION AV647785.1 GI:9868799
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
REFERENCE   1  (bases 1 to 427)
  AUTHORS   Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
            Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
            Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
            Hu,G., Gu,J., Chen,Z. and Han,Z.
  TITLE     Insight into hepatocellular carcinogenesis at transcriptome level
            by comparing gene expression profiles of hepatocellular carcinoma
            with those of corresponding noncancerous liver
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
  MEDLINE   21625106
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="GLCBCA03"
                     /clone_lib="GLC"
                     /tissue_type="corresponding non cancerous liver tissue"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       80 a    149 c    127 g     71 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 9;  Length 427;
  Best Local Similarity   95.0%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||||||||||||||| |
Db    132 CCCCGCCGTGGGTCCGCCTG 151


RESULT 5
BI907636
LOCUS       BI907636                659 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603065545F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214802 5',
            mRNA sequence.
ACCESSION   BI907636
VERSION     BI907636.1  GI:16170473
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 659)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11539  row: i  column: 11
            High quality sequence stop: 655.
FEATURES             Location/Qualifiers
     source          1. .659
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5214802"
                     /clone_lib="NIH_MGC_118"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
BASE COUNT      127 a    198 c    194 g    140 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 10;  Length 659;
  Best Local Similarity   95.0%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||||||||||||||| |
Db    114 CCCCGCCGTGGGTCCGCCTG 133


RESULT 6
BI767868
LOCUS       BI767868                848 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603060993F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5210231 5',
            mRNA sequence.
ACCESSION   BI767868
VERSION     BI767868.1  GI:15759446
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11527  row: j  column: 24
            High quality sequence stop: 845.
FEATURES             Location/Qualifiers
     source          1. .848
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5210231"
                     /clone_lib="NIH_MGC_122"
                     /lab_host="DH10B"
                     /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
                     anonymous pool of 24 week female lung, 16 week female
                     spleen, and 20-22 week male spleens.  Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon  cloning).  Average insert size 1.4 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was  constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking  code 026. Note:
                     this is a NIH_MGC Library."
BASE COUNT      157 a    265 c    230 g    195 t      1 others
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 10;  Length 848;
  Best Local Similarity   95.0%;  Pred. No. 1.2e+03;
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  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||||||||||||||| |
Db    137 CCCCGCCGTGGGTCCGCCTG 156


RESULT 7
BI915042
LOCUS       BI915042                853 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603177231F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5241774 5',
            mRNA sequence.
ACCESSION   BI915042
VERSION     BI915042.1  GI:16179135
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11609  row: m  column: 07
            High quality sequence stop: 840.
FEATURES             Location/Qualifiers
     source          1. .853
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5241774"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      161 a    269 c    229 g    194 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 10;  Length 853;
  Best Local Similarity   95.0%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||||||||||||||| |
Db    125 CCCCGCCGTGGGTCCGCCTG 144


RESULT 8
BI820274
LOCUS       BI820274                885 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603036831F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178031 5',
            mRNA sequence.
ACCESSION   BI820274
VERSION     BI820274.1  GI:15931824
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 885)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11443  row: m  column: 08
            High quality sequence stop: 839.
FEATURES             Location/Qualifiers
     source          1. .885
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5178031"
                     /clone_lib="NIH_MGC_115"
                     /lab_host="DH10B"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
BASE COUNT      172 a    263 c    245 g    205 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 10;  Length 885;
  Best Local Similarity   95.0%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||||||||||||||| |
Db    132 CCCCGCCGTGGGTCCGCCTG 151


RESULT 9
AL553611
LOCUS       AL553611                950 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL553611 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI078YB15 5
            prime, mRNA sequence.
ACCESSION   AL553611
VERSION     AL553611.1  GI:12893606
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 950)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .950
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DI078YB15"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 183 a 291 c 262 g 210 t 4 others
ORIGIN

Query Match 92.0%; Score 18.4; DB 9; Length 950;
Best Local Similarity 95.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCCG 20
||||||||||||||||||| |
Db 112 CCCCGCCGTGGGTCCGCCTG 131

RESULT 10
BG967364/c
LOCUS BG967364 768 bp mRNA linear EST 12-JUN-2001
DEFINITION 602833684F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988205 5', mRNA sequence.
ACCESSION BG967364
VERSION BG967364.1 GI:14355001
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 768)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11000 row: g column: 22
High quality sequence stop: 32.
FEATURES Location/Qualifiers
source 1. .768
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4988205"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 178 a 252 c 205 g 132 t 1 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 768;
Best Local Similarity 94.7%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCC 19
||||||||||||| |||||
Db 677 CCCCGCCGTGGGTGCGCCC 659

RESULT 11
BE619884
LOCUS BE619884 788 bp mRNA linear EST 20-OCT-2000
DEFINITION 601473140T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876321 3', mRNA sequence.
ACCESSION BE619884
VERSION BE619884.1 GI:9890822
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 788)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9636 row: o column: 10
High quality sequence start: 25
High quality sequence stop: 763.
FEATURES Location/Qualifiers
source 1. .788
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3876321"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies. "
BASE COUNT 152 a 236 c 247 g 153 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 788;
Best Local Similarity 94.7%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCC 19
||||||||||| ||||||||
Db 731 CCCCGCCGTGCGTCCGCCC 749

RESULT 12
BG687601/c
LOCUS BG687601 917 bp mRNA linear EST 01-MAY-2001
DEFINITION 602639211F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4762346 5', mRNA sequence.
ACCESSION BG687601
VERSION BG687601.1 GI:13918998
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 917)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

```
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1616  row: e  column: 03
           High quality sequence stop: 191.
FEATURES             Location/Qualifiers
     source          1. .917
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4762346"
                     /clone_lib="NIH_MGC_59"
                     /tissue_type="mucoepidermoid carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
                     Double-stranded cDNA was prepared from cell line RNA.  5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C,  G, or T).  Average
                     insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
                     contained  inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                     Library."
BASE COUNT      231 a    317 c    313 g     56 t
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 10;  Length 917;
  Best Local Similarity   94.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCC 19
          ||||||| ||||||||||
Db    707 CCCCGCCCTGGGTCCGCCC 689


RESULT 13
BF338701/c
LOCUS       BF338701                973 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  602034396F2 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4182406
           5', mRNA sequence.
ACCESSION   BF338701
VERSION     BF338701.1  GI:11285119
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 973)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: David N. Louis, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM9496  row: p  column: 23
           High quality sequence stop: 685.
FEATURES             Location/Qualifiers
     source          1. .973
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4182406"
                     /clone_lib="NCI_CGAP_Brn64"
                     /tissue_type="glioblastoma with EGFR amplification"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.57 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      201 a    304 c    331 g    137 t
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 10;  Length 973;
  Best Local Similarity   94.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCC 19
          |||| ||||||||||||||
Db    798 CCCCCCCGTGGGTCCGCCC 780


RESULT 14
AG162212/c
LOCUS       AG162212                1110 bp    DNA     linear   GSS 09-JAN-2002
DEFINITION  Pan troglodytes DNA, clone: RP43-028J06.TJ, genomic survey
           sequence.
ACCESSION   AG162212
VERSION     AG162212.1  GI:16691890
KEYWORDS    GSS; GSS (genome survey sequence).
SOURCE      Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
           Male BAC Library clone:RP43-028J06.TJ.
  ORGANISM  Pan troglodytes
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (sites)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
           Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library RPCI-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1110)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
           Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
           and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
           1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
           (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
           Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
           end was generated during the R&D process and may have higher chance
           of clone tracking errors.
            PRIMERS
                Sequencing: TJ
            LIBRARY
                Vector    : pBACe3.6
                R.Site 1  : EcoRI
                R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .1110
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="RP43-028J06.TJ"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT      220 a    372 c    493 g     14 t     11 others
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 12;  Length 1110;
  Best Local Similarity   94.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCGCCGTGGGTCCGCCCG 20
          || ||||||||||||||||
Db    576 CCTGCCGTGGGTCCGCCCG 558


RESULT 15
```

```
AW447569/c
LOCUS       AW447569                245 bp    mRNA    linear   EST 25-APR-2001
DEFINITION  89386 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   AW447569
VERSION     AW447569.1  GI:6989356
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 245)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 70  row: B  column: 11
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .245
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 1BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from lymph node, ovary,
                     fat, hypothalamus, and pituitary."
BASE COUNT       54 a     92 c     73 g     26 t
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 9;  Length 245;
  Best Local Similarity   90.0%;  Pred. No. 4.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCCG 20
           |||||||||||| | |||||
Db     224 CCCCGCCGTGGGGCTGCCCG 205


Search completed: November  2, 2002, 17:57:14
Job time : 723.455 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 13:09:44 ; Search time 82.7273 Seconds
(without alignments)
415.078 Million cell updates/sec

Title: US-09-856-803-8
Perfect score: 20
Sequence: 1 ccccgccgtgggtccgcctg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	21	AAA46128	Human beta2 adrene
	2	20	100.0	60	21	AAA38785	Human beta2 adrene
	3	20	100.0	2300	20	AAX61116	Human beta2-adrene
	4	20	100.0	2305	21	AAA38340	Human beta-adrener
	5	20	100.0	3451	20	AAZ00774	Human beta 2-adren
	6	20	100.0	3451	20	AAZ00775	Human beta 2-adren
	7	20	100.0	3451	20	AAZ00777	Human beta 2-adren
	8	20	100.0	3451	20	AAZ00778	Human beta 2-adren
	9	20	100.0	3451	20	AAZ00780	Human beta 2-adren
	10	18.4	92.0	20	21	AAA38788	Human beta2 adrene
	11	18.4	92.0	51	22	AAH79739	Human DNA containi
	12	18.4	92.0	230	22	AAH27139	Human beta-2 adren
	13	18.4	92.0	1999	18	AAT93250	Beta-2 adrenalin r
	14	18.4	92.0	2340	21	AAA38784	Human beta2 adrene
	15	18.4	92.0	3451	19	AAV52614	Human beta-2-adren
	16	18.4	92.0	3451	20	AAZ00776	Human beta 2-adren
	17	18.4	92.0	3451	20	AAZ00779	Human beta 2-adren
	18	18.4	92.0	3451	20	AAZ00773	Human beta 2-adren
	19	18.4	92.0	3451	21	AAA38339	Human beta-adrener
	20	18.4	92.0	3451	24	AAS18444	Reference sequence
c	21	17.4	87.0	1770	22	AAF30281	Perilla flavone sy
	22	16.8	84.0	1057	22	AAI58986	Human polynucleoti
c	23	16.8	84.0	2562	23	ABL03417	Drosophila melanog
c	24	16.8	84.0	9402	23	ABL03416	Drosophila melanog
	25	16.8	84.0	46870	22	AAC82925	S. enterica serova
	26	16.4	82.0	4100	16	AAQ74062	The rat beta-actin
c	27	16	80.0	675	23	ABL13277	Drosophila melanog
c	28	16	80.0	8100	23	ABL13276	Drosophila melanog
	29	15.8	79.0	979	22	AAH98927	Human EST-derived
	30	15.8	79.0	1760	22	AAK94470	Human full-length
	31	15.8	79.0	1880	22	AAK67384	Human immune/haema
c	32	15.8	79.0	6870	21	AAF20955	Interleukin-11 pol
c	33	15.8	79.0	6870	21	AAA34833	Human adenosine re
c	34	15.8	79.0	8055	21	AAF20956	Interleukin-11 pol
c	35	15.8	79.0	8055	21	AAA34834	Human adenosine re
c	36	15.8	79.0	209273	21	AAF21437	Human factor-relat
c	37	15.2	76.0	51	22	AAL33201	Human SNP oligonuc
	38	15.2	76.0	322	22	AAK79152	Human immune/haema
c	39	15.2	76.0	350	22	ABA13458	Human nervous syst
c	40	15.2	76.0	382	22	ABA19596	Human nervous syst
c	41	15.2	76.0	405	22	AAL25605	Human breast cance
	42	15.2	76.0	436	22	AAL05393	Human reproductive
c	43	15.2	76.0	454	22	AAL07859	Human breast cance
	44	15.2	76.0	576	22	AAH05951	Human cDNA clone (
	45	15.2	76.0	589	22	AAH03180	Human cDNA clone (

ALIGNMENTS

RESULT 1
AAA46128
ID AAA46128 standard; DNA; 20 BP.
XX
AC AAA46128;
XX
DT 05-OCT-2000 (first entry)
XX
DE Human beta2 adrenergic receptor beta2AR T allele-specific primer #2.
XX
KW Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW congestive heart failure; ischemic heart disease; arrhythmia;
KW obesity; diabetes; vascular disease; premature labour; migraine;
KW anaphylaxis; chronic obstructive pulmonary disease;
KW allele-specific oligonucleotide primer; ss.
XX
OS Homo sapiens.
XX
PN WO200031307-A1.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US27963.
XX
PR 25-NOV-1998; 98US-0109886.
XX
PA (UYCI-) UNIV CINCINNATI.
XX
PI Liggett SB;
XX
DR WPI; 2000-400107/34.

XX
PT Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT receptor (beta 2 AR), useful for predicting genetic disposition to a
PT disease modified by beta 2 AR expression e.g. congestive heart failure,
PT hypertension -
XX
PS Claim 8; Page 11; 56pp; English.
XX
CC The present sequence is an allele-specific oligonucleotide primer
CC for the T allele of the human beta2 adrenergic receptor (beta2AR) gene,
CC which is located on chromosome 5q31 (12). The gene has two different
CC alleles, and it has been shown that the presence of two copies of the T
CC allele leads to higher expression of the gene. This is because the
CC polymorphism is found in the 5' leader sequence, which encodes a peptide
CC which regulates expression of the beta2AR gene. The polymorphism is
CC thought to affect individuals' responses to beta-agonists and
CC beta-antagonists, and is likely to influence their predisposition to
CC asthma, hypertension, congestive heart failure, ischemic heart disease,
CC arrhythmia, obesity, diabetes, vascular disease, premature labour,
CC migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD).
CC The gene can, therefore, be used to predict the susceptibility of an
CC individual to these diseases and determine the best treatment.
XX
SQ Sequence 20 BP; 0 A; 10 C; 7 G; 3 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCTG 20
||||||||||||||||||||
Db 1 CCCCGCCGTGGGTCCGCCTG 20

RESULT 2
AAA38785
ID AAA38785 standard; DNA; 60 BP.
XX
AC AAA38785;
XX
DT 05-OCT-2000 (first entry)
XX
DE Human beta2 adrenergic receptor beta2AR gene fragment.
XX
KW Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW congestive heart failure; ischemic heart disease; arrhythmia;
KW obesity; diabetes; vascular disease; premature labour; migraine;
KW anaphylaxis; chronic obstructive pulmonary disease; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT allele replace(55,C)
FT /*tag= a
XX
PN WO200031307-A1.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US27963.
XX
PR 25-NOV-1998; 98US-0109886.
XX
PA (UYCI-) UNIV CINCINNATI.
XX
PI Liggett SB;
XX
DR WPI; 2000-400107/34.
DR P-PSDB; AAY99531.
XX
PT Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT receptor (beta 2 AR), useful for predicting genetic disposition to a
PT disease modified by beta 2 AR expression e.g. congestive heart failure,
PT hypertension -
XX
PS Disclosure; Figure 2; 56pp; English.
XX
CC The present sequence is a fragment of the T allele of the human beta2
CC adrenergic receptor (beta2AR) gene, which is located on chromosome
CC 5q31 (12). The gene has two different alleles, and it has been shown that
CC the presence of two copies of the T allele leads to higher expression of
CC the gene. This is because the polymorphism is found in the 5' leader
CC sequence, which encodes a peptide which regulates expression of the
CC beta2AR gene. The polymorphism is thought to affect individuals'
CC responses to beta-agonists and beta-antagonists, and is likely to
CC influence their predisposition to asthma, hypertension,
CC congestive heart failure, ischemic heart disease, arrhythmia, obesity,
CC diabetes, vascular disease, premature labour, migraine, anaphylaxis and
CC chronic obstructive pulmonary disease (COPD). The gene can, therefore, be
CC used to predict the susceptibility of an individual to these diseases and
CC determine the best treatment.
XX
SQ Sequence 60 BP; 6 A; 24 C; 21 G; 9 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCTG 20
||||||||||||||||||||
Db 37 CCCCGCCGTGGGTCCGCCTG 56

RESULT 3
AAX61116
ID AAX61116 standard; DNA; 2300 BP.
XX
AC AAX61116;
XX
DT 27-JUL-1999 (first entry)
XX
DE Human beta2-adrenergic receptor gene.
XX
KW Alpha1B-adrenergic receptor; human; cardiovascular disease;
KW beta2 adrenergic receptor; genetic variation identification; hypertrophy;
KW disease diagnosis; hypertension; prostatic disease; pulmonary disorder;
KW asthma; peripheral vascular disorder; neuropsychic disorder;
KW endocrine-metabolic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO9924454-A1.
XX
PD 20-MAY-1999.
XX
PF 04-NOV-1998; 98WO-US23496.
XX
PR 10-NOV-1997; 97US-0086232.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Buescher R, Herrmann V, Insel PA;
XX
DR WPI; 1999-327357/27.
XX
PT Pairs of oligonucleotides for amplifying adrenergic receptor genes
XX
PS Disclosure; Fig 2; 58pp; English.
XX
CC This sequence represents the human beta2-adrenergic receptor gene, and
CC is amplified by the primers of the invention. The primers are non-self
CC hybridising; contain at least 15 nucleotides (nt) and has a melting
CC temperature 50-85 deg. C. Each pair of primers is: non-cross-hybridising;
CC anneals to two distinct segments (separated by at least 400 nt); and
CC generates a homogeneous population of gene segments in a polymerase chain

CC reaction (PCR). At least one primer in the pair can extend a 3'-end
CC sequence complementary to a template sequence in a DNA polymerase
CC reaction. The primers are used to amplify segments of the alpha1B and
CC beta2 adrenergic receptor genes, particularly to identify genetic
CC variations for diagnosis of disease. Specifically variations in the
CC alpha1B gene are associated with cardiovascular disease, hypertension and
CC prostatic disease (hypertrophy), and those in the beta2 gene with
CC cardiovascular disease, hypertension and asthma, but variations may also
CC be associated with peripheral vascular, pulmonary, neuropsychic and
CC endocrine-metabolic disorders. These primers allow rapid and specific
CC amplification of large and homogeneous gene segments of the alpha1B and
CC beta2 genes from a complex mixture of DNAs. This makes possible detection
CC of genetic alterations not previously amenable to routine, automated and
CC large-scale sequencing analysis.
XX
SQ Sequence 2300 BP; 495 A; 613 C; 646 G; 546 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 2300;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCTG 20
||||||||||||||||||||
Db 729 CCCCGCCGTGGGTCCGCCTG 748

RESULT 4
AAA38340
ID AAA38340 standard; DNA; 2305 BP.
XX
AC AAA38340;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human beta-adrenergic receptor-2 coding region.
XX
KW Beta-adrenergic receptor-2 gene; coding region;
KW polymorphism; polymorphic marker; cardiovascular disease;
KW myocardial infarction; unstable angina; hypertension; atherosclerosis;
KW stroke; prognosis; drug screening; treatment outcome; human; ds.
XX
OS Homo sapiens.
XX
PN WO200022166-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-IB01678.
XX
PR 14-OCT-1998; 98US-0104286.
PR 14-OCT-1998; 98US-0104302.
XX
PA (EURO-) EURONA MEDICAL AB.
XX
PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
XX
DR WPI; 2000-318010/27.
XX
PT Assessing cardiovascular status in humans involves comparing test
PT polymorphic pattern comprising polymorphic positions within genes
PT encoding specific proteins, with reference polymorphic pattern -
XX
PS Disclosure; Page 124-125; 126pp; English.
XX
CC The invention relates to a novel method of assessing the cardiovascular
CC status in an individual and to newly identified polymorphisms in the
CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II
CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
CC aldosterone synthase, endothelin receptor type A and beta-adrenergic
CC receptors 1 and 2. The method comprises determining the sequence at one
CC or more polymorphic positions within these genes, and comparing the
CC pattern of polymorphisms from the individual with a reference polymorphic
CC pattern obtained from a population of individuals exhibiting a
CC predetermined cardiovascular disease status. The polymorphic markers are
CC useful for determining the predisposition of an individual to
CC cardiovascular disorders such as myocardial infarction, unstable angina,
CC hypertension, atherosclerosis and stroke. They are also useful for
CC predicting the likely cardiovascular status of a patient given a
CC treatment regimen comprising administration of cardiovascular drugs
CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
CC blockers) or calcium channel blockers). One or more polymorphic markers
CC provides a basis for predicting the outcome of a treatment regimen.
CC Fragments of the genes comprising a polymorphic site may be used as
CC primers and probes for detecting genetic polymorphisms or in molecular
CC library arrays for high throughput screening. The genes, and the proteins
CC they encode are useful in the screening of potential cardiovascular
CC drugs. Determination of an individual's polymorphic pattern reduces or
CC eliminates trial and error in selecting a treatment for a particular
CC individual cardiovascular patient. It also provides the ability to
CC eliminate patients from clinical trials who are predicted to be
CC non-responsive, or at a risk for an adverse response, to a particular
CC treatment regimen. Adverse results in an early trial can be evaluated to
CC identify polymorphic patterns so that the adverse results can be
CC correlated with a sub-population of the test population, permitting
CC exclusion of such sub-populations from the treatment group. Beneficial
CC drugs can be approved for use in the appropriate population, thereby
CC decreasing the number of patients required for a clinical trial, which in
CC turn decreases the duration and cost of such trials. The present
CC sequence represents the human beta-adrenergic receptor-2 gene
CC coding region (GenBank Y00106/g293708). The polymorphic sites identified
CC are 839A/G, 872C/G, 1045A/G, 1284C/T, 1316A/C, 1846C/G, 2032A/G,
CC 2068 no insert/G/C and 2070 no insert/C.
XX
SQ Sequence 2305 BP; 495 A; 616 C; 649 G; 545 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 2305;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCTG 20
||||||||||||||||||||
Db 729 CCCCGCCGTGGGTCCGCCTG 748

RESULT 5
AAZ00774
ID AAZ00774 standard; DNA; 3451 BP.
XX
AC AAZ00774;
XX
DT 07-OCT-1999 (first entry)
XX
DE Human beta 2-adrenergic receptor DNA variant 1.
XX
KW Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW cardiovascular disease; myocardial infarction; anxiety; depression;
KW neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW post-traumatic stress disorder; autonomous nervous system disease;
KW metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation replace(159,t)
FT /*tag= a
FT /note= "This nucleotide differs from the wild type
FT nucleic acid sequence represented in AAZ00773"
FT mutation replace(245,a)
FT /*tag= b
FT /note= "This nucleotide differs from the wild type
FT nucleic acid sequence represented in AAZ00773"
FT mutation replace(565,g)

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FT                  /*tag= c
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation       replace(934,g)
FT                  /*tag= d
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation       replace(1120,g)
FT                  /*tag= e
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation       replace(1221,c)
FT                  /*tag= f
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation       replace(1541,t)
FT                  /*tag= g
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773
FT                         and results in a change in the corresponding
FT                         wild type amino acid sequence from an Cys
FT                         residue to Arg residue"
FT   mutation       replace(1568,t)
FT                  /*tag= h
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation       replace(1633,a)
FT                  /*tag= i
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773
FT                         and results in a change in the corresponding
FT                         wild type amino acid sequence from an Gly
FT                         residue to Arg residue"
FT   mutation       replace(1666,c)
FT                  /*tag= j
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773
FT                         and results in a change in the corresponding
FT                         wild type amino acid sequence from an Glu
FT                         residue to Gln residue"
FT   mutation       replace(1839,g)
FT                  /*tag= k
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation       replace(2078,c)
FT                  /*tag= l
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773
FT                         and results in a change in the corresponding
FT                         wild type amino acid sequence from an Ile
FT                         residue to Thr residue"
FT   mutation       replace(2110,c)
FT                  /*tag= m
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation       replace(2640,g)
FT                  /*tag= n
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT   mutation       replace(2826,g)
FT                  /*tag= o
FT                  /note= "This nucleotide differs from the wild type
FT                         nucleic acid sequence represented in AAZ00773"
FT
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 2; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 794 A; 871 C; 892 G; 894 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||||||||
Db   1523 CCCCGCCGTGGGTCCGCCTG 1542


RESULT 6
AAZ00775
ID   AAZ00775 standard; DNA; 3451 BP.
XX
AC   AAZ00775;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 2.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1541,c)
FT                   /*tag= a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
XX
```

```
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 3; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 790 A; 872 C; 895 G; 894 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||||||||
Db   1523 CCCCGCCGTGGGTCCGCCTG 1542


RESULT 7
AAZ00777
ID   AAZ00777 standard; DNA; 3451 BP.
XX
AC   AAZ00777;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 4.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1541,c)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
FT   mutation        replace(1633,a)
FT                   /*tag=  b
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 5; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 789 A; 872 C; 896 G; 894 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||||||||
Db   1523 CCCCGCCGTGGGTCCGCCTG 1542


RESULT 8
AAZ00778
ID   AAZ00778 standard; DNA; 3451 BP.
XX
AC   AAZ00778;
XX
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DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 5.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1541,c)
FT                   /*tag= a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 6; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 790 A; 872 C; 895 G; 894 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           ||||||||||||||||||||

Db    1523 CCCCGCCGTGGGTCCGCCTG 1542


RESULT 9
AAZ00780
ID   AAZ00780 standard; DNA; 3451 BP.
XX
AC   AAZ00780;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 7.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1541,t)
FT                   /*tag= g
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
FT   mutation        replace(1633,a)
FT                   /*tag= b
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 8; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
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CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 789 A; 872 C; 896 G; 894 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||||||||
Db   1523 CCCCGCCGTGGGTCCGCCTG 1542


RESULT 10
AAA38788
ID   AAA38788 standard; DNA; 20 BP.
XX
AC   AAA38788;
XX
DT   05-OCT-2000  (first entry)
XX
DE   Human beta2 adrenergic receptor beta2AR C allele-specific primer #1.
XX
KW   Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW   chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW   congestive heart failure; ischemic heart disease; arrhythmia;
KW   obesity; diabetes; vascular disease; premature labour; migraine;
KW   anaphylaxis; chronic obstructive pulmonary disease;
KW   allele-specific oligonucleotide primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200031307-A1.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US27963.
XX
PR   25-NOV-1998;   98US-0109886.
XX
PA   (UYCI-) UNIV CINCINNATI.
XX
PI   Liggett SB;
XX
DR   WPI; 2000-400107/34.
XX
PT   Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT   receptor (beta 2 AR), useful for predicting genetic disposition to a
PT   disease modified by beta 2 AR expression e.g. congestive heart failure,
PT   hypertension -
XX
PS   Claim 8; Page 11; 56pp; English.
XX
CC   The present sequence is an allele-specific oligonucleotide primer
CC   for the C allele of the human beta2 adrenergic receptor (beta2AR) gene,
CC   which is located on chromosome 5q31 (12). The gene has two different
CC   alleles, and it has been shown that the presence of two copies of the T
CC   allele leads to higher expression of the gene. This is because the
CC   polymorphism is found in the 5' leader sequence, which encodes a peptide
CC   which regulates expression of the beta2AR gene. The polymorphism is
CC   thought to affect individuals' responses to beta-agonists and
CC   beta-antagonists, and is likely to influence their predisposition to
CC   asthma, hypertension, congestive heart failure, ischemic heart disease,
CC   arrhythmia, obesity, diabetes, vascular disease, premature labour,
CC   migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD).
CC   The gene can, therefore, be used to predict the susceptibility of an
CC   individual to these diseases and determine the best treatment.
XX
SQ   Sequence 20 BP; 0 A; 11 C; 7 G; 2 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 21;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 47;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          |||||||||||||||||| |
Db      1 CCCCGCCGTGGGTCCGCCCG 20


RESULT 11
AAH79739
ID   AAH79739 standard; DNA; 51 BP.
XX
AC   AAH79739;
XX
DT   19-SEP-2001  (first entry)
XX
DE   Human DNA containing single nucleotide polymorphism SEQ ID NO. 354.
XX
KW   Human; single nucleotide polymorphism; SNP; angiopoietin;
KW   4-hydroxybutyrate; dehydrogenase; protein therapy;
KW   adenosine triphosphate-dependent RNA helicase;
KW   major histocompatibility complex Class I histocompatibility antigen; MHC;
KW   phosphoglycerate kinase; immunosuppressive; immunostimulatory;
KW   antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
KW   antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; ds.
XX
OS   Homo sapiens.
XX
PN   WO200148245-A2.
XX
PD   05-JUL-2001.
XX
PF   27-DEC-2000; 2000WO-US35346.
XX
PR   27-DEC-1999;   99US-0472688.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-418297/44.
XX
PT   Polymorphic nucleic acids encoding e.g. angiopoietin, dehydrogenase,
PT   adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
PT   kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
PT   diseases and infections -
XX
PS   Claim 1; Page 162; 484pp; English.
XX
CC   The invention relates to nucleic acids (AAH79386-AAH80036) encoding
CC   polymorphic variants of proteins (AAG98010-AAG98238) related to
CC   angiopoietin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
CC   (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
CC   Class I histocompatibility antigen and/or phosphoglycerate kinase. These
CC   nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
CC   proteins have potential immunosuppressive, immunostimulatory,
CC   antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
CC   antileukemic, neuroprotective and antimicrobial activity and may be
CC   useful in gene/protein therapy, vaccines, modulation of the expression
CC   and activity of proteins related to angiopoietin, 4-hydroxybutyrate,
CC   dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase,
CC   major histocompatibility complex (MHC) Class I histocompatibility antigen
CC   and/or phosphoglycerate kinase. Disorders that may be prevented,
CC   diagnosed and/or treated by the above methods include multifactorial
CC   diseases with a genetic component, such as autoimmune diseases (e.g.
CC   rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
CC   erytheromatosus and Grave's disease), inflammation, cancer (e.g. cancers
CC   of the bladder, brain, breast, colon and kidney, leukemia), diseases of
CC   the nervous system, an infection of pathogenic organisms. They may also
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CC   be used to alter phenotypic traits such as longevity, appearance,
CC   strength, speed and endurance.
XX
SQ   Sequence 51 BP; 5 A; 24 C; 18 G; 4 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 22;  Length 51;
  Best Local Similarity   95.0%;  Pred. No. 44;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          |||||||||||||||||| |
Db      8 CCCCGCCGTGGGTCCGCCCG 27


RESULT 12
AAH27139
ID   AAH27139 standard; DNA; 230 BP.
XX
AC   AAH27139;
XX
DT   08-AUG-2001  (first entry)
XX
DE   Human beta-2 adrenergic receptor UTR region with RBP binding ability.
XX
KW   Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration;
KW   stroke; cardiovascular disease; hypertension; cancer; inflammation;
KW   metabolic disorder; obesity; diabetes; beta-2 adrenergic receptor; ds.
XX
OS   Homo sapiens.
XX
PN   WO200134624-A1.
XX
PD   17-MAY-2001.
XX
PF   09-NOV-2000; 2000WO-US30888.
XX
PR   10-NOV-1999;   99US-0437458.
XX
PA   (MESS-) MESSAGE PHARM INC.
XX
PI   Giordano A,  Xavier AK;
XX
DR   WPI; 2001-335904/35.
XX
PT   New nucleic acids that bind RNA-binding proteins or regulate mRNA
PT   function, useful for therapeutic gene regulation, such as in cases of
PT   neurodegeneration  -
XX
PS   Claim 1; Page 28; 33pp; English.
XX
CC   Sequences AAH27132 - AAH27151 represent human gene untranslated regions
CC   where the corresponding mRNA fragment has RNA binding protein (RBP)
CC   binding activity. RBPs mediate the processing of pre-mRNA, the transport
CC   of mRNA from the nucleus to the cytoplasm, mRNA stabilisation,
CC   translational efficiency, and the sequestration of some mRNAs. Therefore
CC   modification of post-transcriptional protein expression in eukaryotic
CC   cells may be carried out through the targeting specific interactions of
CC   proteins that bind to RBPs. The gene fragments of the invention are used
CC   to identify their optimized sub-fragments, compounds that affect RNA/RBP
CC   interaction or mRNA functionality; or RBPs that interact with the
CC   compounds. Compounds identified using the gene fragments are potentially
CC   useful for therapeutic regulation of gene expression, such as in cases of
CC   neurodegeneration; stroke; cardiovascular disease; hypertension; cancer;
CC   inflammation; metabolic disorders (obesity and diabetes) and bacterial or
CC   viral infection. The present sequence is one of gene fragments of the
CC   invention, isolated from the human beta-2 adrenergic receptor gene.
XX
SQ   Sequence 230 BP; 42 A; 91 C; 70 G; 27 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 22;  Length 230;
  Best Local Similarity   95.0%;  Pred. No. 39;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          |||||||||||||||||| |
Db    155 CCCCGCCGTGGGTCCGCCCG 174


RESULT 13
AAT93250
ID   AAT93250 standard; cDNA to mRNA; 1999 BP.
XX
AC   AAT93250;
XX
DT   20-APR-1998  (first entry)
XX
DE   Beta-2 adrenalin receptor subtype coding sequence.
XX
KW   Beta-2 adrenalin subtype; cyanopindrol; agonist; antagonist;
KW   asthmatic disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             190..1431
FT                   /*tag=  a
XX
PN   WO9735963-A1.
XX
PD   02-OCT-1997.
XX
PF   24-MAR-1997;   97WO-JP00982.
XX
PR   27-MAR-1996;   96JP-0072914.
XX
PA   (DAIN ) DAINIPPON PHARM CO LTD.
XX
PI   Fujii K,  Furutani Y,  Kawashima H,  Nomura A,  Yano K;
XX
DR   WPI; 1997-489627/45.
DR   P-PSDB; AAW34320.
XX
PT   Novel beta-2 adrenalin receptor sub-type - useful for screening for
PT   agonists and antagonists and researching asthmatic diseases
XX
PS   Disclosure; Page 27-30; 47pp; Japanese.
XX
CC   This sequence encodes the protein of the invention. The protein of the
CC   invention is a beta-2 adrenalin receptor subtype with Kd value of
CC   approximately 75 pM against 125I-cyanopindrol. The protein can be used in
CC   screening for agonists and antagonists, which are useful in researching
CC   asthmatic diseases.
XX
SQ   Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 18;  Length 1999;
  Best Local Similarity   95.0%;  Pred. No. 33;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          |||||||||||||||||| |
Db    125 CCCCGCCGTGGGTCCGCCCG 144


RESULT 14
AAA38784
ID   AAA38784 standard; DNA; 2340 BP.
XX
AC   AAA38784;
XX
DT   05-OCT-2000  (first entry)
XX
DE   Human beta2 adrenergic receptor beta2AR gene.
XX
KW   Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW   chromosome 5q31(12); disease predisposition; asthma; hypertension;
```

```
KW   congestive heart failure; ischemic heart disease; arrhythmia;
KW   obesity; diabetes; vascular disease; premature labour; migraine;
KW   anaphylaxis; chronic obstructive pulmonary disease; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1487..2340
FT                   /*tag= a
FT                   /product= "beta2 adrenergic receptor"
FT                   /note= "no stop codon given at 3' end of sequence"
FT                   /partial
FT   sig_peptide     1487..1546
FT                   /*tag= b
FT                   /label= 5'_leader_cistron
FT   allele          replace(1541,T)
FT                   /*tag= c
FT   mat_peptide     1588..2340
FT                   /*tag= d
XX
PN   WO200031307-A1.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US27963.
XX
PR   25-NOV-1998;   98US-0109886.
XX
PA   (UYCI-) UNIV CINCINNATI.
XX
PI   Liggett SB;
XX
DR   WPI; 2000-400107/34.
XX
PT   Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT   receptor (beta 2 AR), useful for predicting genetic disposition to a
PT   disease modified by beta 2 AR expression e.g. congestive heart failure,
PT   hypertension -
XX
PS   Disclosure; Figure 1; 56pp; English.
XX
CC   The present sequence is a fragment of the C allele of the human beta2
CC   adrenergic receptor (beta2AR) gene, which is located on chromosome
CC   5q31 (12). The gene has two different alleles, and it has been shown that
CC   the presence of two copies of the T allele leads to higher expression of
CC   the gene. This is because the polymorphism is found in the 5' leader
CC   sequence, which encodes a peptide which regulates expression of the
CC   beta2AR gene. The polymorphism is thought to affect individuals'
CC   responses to beta-agonists and beta-antagonists, and is likely to
CC   influence their predisposition to asthma, hypertension,
CC   congestive heart failure, ischemic heart disease, arrhythmia, obesity,
CC   diabetes, vascular disease, premature labour, migraine, anaphylaxis and
CC   chronic obstructive pulmonary disease (COPD). The gene can, therefore, be
CC   used to predict the susceptibility of an individual to these diseases and
CC   determine the best treatment.
XX
SQ   Sequence 2340 BP; 498 A; 627 C; 653 G; 562 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 21;  Length 2340;
  Best Local Similarity   95.0%;  Pred. No. 33;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||||||||||||||| |
Db    1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 15
AAV52614
ID   AAV52614 standard; cDNA; 3451 BP.
XX
AC   AAV52614;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Human beta-2-adrenergic receptor cDNA.
XX
KW   Beta-2-adrenergic receptor; human; asthma; beta-agonist;
KW   polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1588..2829
FT                   /*tag= a
FT   variation       1633
FT                   /*tag= b
FT                   /note= "A to G substitution, results in Arg16
FT                           to Gly amino acid change"
XX
PN   WO9839477-A2.
XX
PD   11-SEP-1998.
XX
PF   26-FEB-1998;   98WO-US03908.
XX
PR   03-MAR-1997;   97US-0811441.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Boushey H,  Chinchilli VM,  Drazen JM,  Fish JE,  Ford JG;
PI   Martin RJ;
XX
DR   WPI; 1998-506372/43.
DR   P-PSDB; AAW75777.
XX
PT   Diagnosing asthma patients predisposed to adverse beta-agonist
PT   reactions upon regular administration - by identifying patients
PT   homozygous for allele encoding Arg at position 16 of
PT   beta2-adrenergic receptor protein
XX
PS   Disclosure; Page 33-35; 46pp; English.
XX
CC   This cDNA sequence codes for human beta-2-adrenergic receptor (see
CC   AAW75777) having an arginine residue at position 16.  A novel method
CC   for identifying individuals susceptible to adverse responses to
CC   regular administration of beta-agonists comprises: (a) identifying
CC   in a genomic nucleic acid sample from the individual first and
CC   second alleles of the beta 2-adrenergic receptor gene, and (b)
CC   classifying an individual as susceptible if first and second
CC   alleles both encode Arg at residue 16 of the beta 2-adrenergic
CC   receptor protein.  Beta 2-adrenergic receptor gene alleles may be
CC   identified by any known method e.g. denaturing gel electrophoresis
CC   or PCR amplification (see also AAV52615-17).  Identification
CC   preferably comprises amplifying a portion of each allele which
CC   includes the sequence encoding residue 16, and optionally also
CC   comprises determining nucleotide sequences of these portions (e.g.
CC   by automated sequence analysis).  The invention identifies a known
CC   polymorphism in the beta 2-adrenergic receptor gene as being linked
CC   to adverse responses to regular beta-agonist administration;
CC   position 16 of the encoded protein can be either Arg or Gly, and
CC   individuals homozygous for Arg16 are more susceptible.
XX
SQ   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 19;  Length 3451;
  Best Local Similarity   95.0%;  Pred. No. 32;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||||||||||||||| |
Db    1523 CCCCGCCGTGGGTCCGCCCG 1542


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Job time : 83.7273 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 14:22:04 ; Search time 18.5455 Seconds
(without alignments)
264.899 Million cell updates/sec

Title: US-09-856-803-8
Perfect score: 20
Sequence: 1 ccccgccgtgggtccgcctg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18.4	92.0	230	4	US-09-437-457-8	Sequence 8, Appli
c	2	15.4	77.0	1730	6	5223391-8	Patent No. 5223391
	3	15.2	76.0	684	3	US-09-181-183-31	Sequence 31, Appl
	4	15.2	76.0	684	4	US-09-277-700-31	Sequence 31, Appl
c	5	15.2	76.0	830	3	US-09-165-240-1	Sequence 1, Appli
c	6	15.2	76.0	830	4	US-09-568-059-1	Sequence 1, Appli
c	7	15.2	76.0	833	3	US-09-165-240-2	Sequence 2, Appli
c	8	15.2	76.0	833	4	US-09-568-059-2	Sequence 2, Appli
	9	15.2	76.0	1876	1	US-08-483-232-24	Sequence 24, Appl
	10	15.2	76.0	1876	2	US-08-485-938A-24	Sequence 24, Appl
	11	15.2	76.0	1876	2	US-08-910-041-24	Sequence 24, Appl
	12	15.2	76.0	1876	3	US-09-328-474-24	Sequence 24, Appl
	13	15.2	76.0	1876	3	US-09-100-546-24	Sequence 24, Appl
	14	15.2	76.0	1876	3	US-09-010-715-24	Sequence 24, Appl
	15	15.2	76.0	1876	4	US-09-577-758-24	Sequence 24, Appl
c	16	15.2	76.0	2119	4	US-09-018-635-28	Sequence 28, Appl
c	17	15.2	76.0	2253	6	5457037-2	Patent No. 5457037
	18	15.2	76.0	2350	4	US-09-187-478-1	Sequence 1, Appli
	19	15.2	76.0	2350	4	US-09-292-036-1	Sequence 1, Appli
c	20	15.2	76.0	2625	6	5457037-4	Patent No. 5457037
	21	15.2	76.0	2877	2	US-08-317-401E-1	Sequence 1, Appli
c	22	15.2	76.0	3336	6	5457037-1	Patent No. 5457037
c	23	14.4	72.0	1873	4	US-09-011-540-1	Sequence 1, Appli
c	24	14.2	71.0	480	5	PCT-US95-08295-18	Sequence 18, Appl
c	25	14.2	71.0	652	1	US-08-034-650-13	Sequence 13, Appl
c	26	14.2	71.0	652	1	US-08-034-650-12	Sequence 13, Appl
c	27	14.2	71.0	660	1	US-08-449-015-13	Sequence 12, Appl
c	28	14.2	71.0	660	1	US-08-449-015-12	Sequence 12, Appl
c	29	14.2	71.0	1078	2	US-08-874-186-36	Sequence 36, Appl
	30	14.2	71.0	1247	1	US-08-278-729A-32	Sequence 32, Appl
	31	14.2	71.0	1247	1	US-08-155-343A-32	Sequence 32, Appl
	32	14.2	71.0	1247	1	US-08-406-672-32	Sequence 32, Appl
	33	14.2	71.0	1247	1	US-08-643-563A-32	Sequence 32, Appl
	34	14.2	71.0	1247	1	US-08-643-763A-32	Sequence 32, Appl
	35	14.2	71.0	1247	1	US-08-462-623-32	Sequence 32, Appl
	36	14.2	71.0	1247	1	US-08-451-953A-32	Sequence 32, Appl
	37	14.2	71.0	1247	2	US-08-445-468A-32	Sequence 32, Appl
	38	14.2	71.0	1247	2	US-08-461-397A-32	Sequence 32, Appl
	39	14.2	71.0	1247	2	US-08-912-088-32	Sequence 32, Appl
	40	14.2	71.0	1247	3	US-08-278-730A-32	Sequence 32, Appl
	41	14.2	71.0	1247	3	US-08-445-467-32	Sequence 32, Appl
	42	14.2	71.0	1247	3	US-08-480-515A-32	Sequence 32, Appl
	43	14.2	71.0	1247	4	US-09-170-936-32	Sequence 32, Appl
	44	14.2	71.0	1247	5	PCT-US93-07190-32	Sequence 32, Appl
	45	14.2	71.0	1247	5	PCT-US93-07231-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-437-457-8
; Sequence 8, Application US/09437457
; Patent No. 6273893
; GENERAL INFORMATION:
; APPLICANT: Giordano, Anthony
; APPLICANT: Xavier, Ashish
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
; TITLE OF INVENTION: INTERACTIONS AND MRNA FUNCTIONALITY
; FILE REFERENCE: 50093/014001
; CURRENT APPLICATION NUMBER: US/09/437,457
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-437-457-8

Query Match 92.0%; Score 18.4; DB 4; Length 230;
Best Local Similarity 95.0%; Pred. No. 6.7;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCTG 20
||||||||||||||||||| |
Db 155 CCCCGCCGTGGGTCCGCCCG 174

RESULT 2
5223391-8/c
;Patent No. 5223391
; APPLICANT: COEN, DONALD M.;DIGARD, PAUL E.
; TITLE OF INVENTION: INHIBITIORS OF HERPES SIMPLEX VIRUS
;REPLICATION
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,634
; FILING DATE: 21-FEB-1990
;SEQ ID NO:8:
; LENGTH: 1730
5223391-8

Query Match 77.0%; Score 15.4; DB 6; Length 1730;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGC 17
| |||||||||||||||

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Db     464 CGCCGCCGTGGGTCCGC 448


RESULT 3
US-09-181-183-31
; Sequence 31, Application US/09181183
; Patent No. 6146866
;  GENERAL INFORMATION:
;    APPLICANT:  VIITANEN, PAUL VEIKKO
;    APPLICANT:  BACOT, KAREN ONLEY
;    APPLICANT:  JORDAN, DOUGLAS BRIAN
;    TITLE OF INVENTION:  LUMAZINE SYNTHASE AND
;    TITLE OF INVENTION:  RIBOFLAVIN SYNTHASE
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. DU PONT DE NEMOURS AND COMPANY
;      STREET:  1007 MARKET STREET
;      CITY:  WILMINGTON
;      STATE:  DELAWARE
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.50 INCH
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  MICROSOFT WORD FOR WINDOWS 95
;      SOFTWARE:  MICROSOFT WORD VERSION 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/181,183
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FLOYD, LINDA AXAMETHY
;      REGISTRATION NUMBER:  33,692
;      REFERENCE/DOCKET NUMBER:  CL-1083
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-8112
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  684 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  arabidopsis LS precursor
US-09-181-183-31

  Query Match           76.0%;  Score 15.2;  DB 3;  Length 684;
  Best Local Similarity  85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           | ||||||||  ||||||||
Db      17 CGCCGCCGTGTCTCCGCCTG 36


RESULT 4
US-09-277-700-31
; Sequence 31, Application US/09277700
; Patent No. 6350597
; GENERAL INFORMATION:
;  APPLICANT: VIITANEN, PAUL V.
;  APPLICANT: BACOT, KAREN O.
;  APPLICANT: JORDAN, DOUGLAS B.
;  TITLE OF INVENTION: RIBOFLAVIN SYNTHASE GENES AND ENZYMES
;  TITLE OF INVENTION: AND METHODS OF USE
;  FILE REFERENCE: CL-1083-B
;  CURRENT APPLICATION NUMBER: US/09/277,700
;  CURRENT FILING DATE: 1999-03-26
;  EARLIER APPLICATION NUMBER: 08/912,218
;  EARLIER FILING DATE: AUGUST 15, 1997
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 31
;    LENGTH: 684
;    TYPE: DNA
;    ORGANISM: arabidopsis
US-09-277-700-31

  Query Match           76.0%;  Score 15.2;  DB 4;  Length 684;
  Best Local Similarity  85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           | ||||||||  ||||||||
Db      17 CGCCGCCGTGTCTCCGCCTG 36


RESULT 5
US-09-165-240-1/c
; Sequence 1, Application US/09165240A
; Patent No. 6087164
; GENERAL INFORMATION:
;  APPLICANT: Hochberg, Abraham
;  APPLICANT: Ayesh, Suhail
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
;  TITLE OF INVENTION: TUMOR-SPECIFIC CYTOTOXICITY
;  FILE REFERENCE: 9457-0014-999
;  CURRENT APPLICATION NUMBER: US/09/165,240A
;  CURRENT FILING DATE: 1998-10-01
;  EARLIER APPLICATION NUMBER: US 08/943,608
;  EARLIER FILING DATE: 1997-10-03
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;    LENGTH: 830
;    TYPE: DNA
;    ORGANISM: Homo Sapien
US-09-165-240-1

  Query Match           76.0%;  Score 15.2;  DB 3;  Length 830;
  Best Local Similarity  85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||| |||||||||  | |
Db      62 CCCCGCTGTGGGTCCGTCGG 43


RESULT 6
US-09-568-059-1/c
; Sequence 1, Application US/09568059
; Patent No. 6306833
; GENERAL INFORMATION:
;  APPLICANT:  Hochberg, Abraham
;  APPLICANT:  Ayesh, Suhail
;  TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR INDUCING
;  TITLE OF INVENTION:  TUMOR-SPECIFIC CYTOTOXICITY
;  FILE REFERENCE:  9457-0014-999
;  CURRENT APPLICATION NUMBER: US/09/568,059
;  CURRENT FILING DATE:  2000-05-10
;  PRIOR APPLICATION NUMBER:  09/165,240
;  PRIOR FILING DATE:  1998-10-01
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 830
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-568-059-1

  Query Match           76.0%;  Score 15.2;  DB 4;  Length 830;
  Best Local Similarity  85.0%;  Pred. No. 1.4e+02;
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  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||| ||||||||| | |
Db      62 CCCCGCTGTGGGTCCGTCGG 43


RESULT 7
US-09-165-240-2/c
; Sequence 2, Application US/09165240A
; Patent No. 6087164
; GENERAL INFORMATION:
;  APPLICANT: Hochberg, Abraham
;  APPLICANT: Ayesh, Suhail
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
;  TITLE OF INVENTION: TUMOR-SPECIFIC CYTOTOXICITY
;  FILE REFERENCE: 9457-0014-999
;  CURRENT APPLICATION NUMBER: US/09/165,240A
;  CURRENT FILING DATE: 1998-10-01
;  EARLIER APPLICATION NUMBER: US 08/943,608
;  EARLIER FILING DATE: 1997-10-03
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 833
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-165-240-2

  Query Match             76.0%;  Score 15.2;  DB 3;  Length 833;
  Best Local Similarity   85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||| ||||||||| | |
Db      50 CCCCGCTGTGGGTCCGTCGG 31


RESULT 8
US-09-568-059-2/c
; Sequence 2, Application US/09568059
; Patent No. 6306833
; GENERAL INFORMATION:
;  APPLICANT:  Hochberg, Abraham
;  APPLICANT:  Ayesh, Suhail
;  TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR INDUCING
;  TITLE OF INVENTION:  TUMOR-SPECIFIC CYTOTOXICITY
;  FILE REFERENCE:  9457-0014-999
;  CURRENT APPLICATION NUMBER: US/09/568,059
;  CURRENT FILING DATE:  2000-05-10
;  PRIOR APPLICATION NUMBER:  09/165,240
;  PRIOR FILING DATE:  1998-10-01
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 833
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-568-059-2

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 833;
  Best Local Similarity   85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||| ||||||||| | |
Db      50 CCCCGCTGTGGGTCCGTCGG 31


RESULT 9
US-08-483-232-24
; Sequence 24, Application US/08483232
; Patent No. 5656431
;  GENERAL INFORMATION:
;    APPLICANT:  Cousens, Lawrence S.
;    APPLICANT:  Eberhardt, Christine D.
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Le Trong, Hai
;    APPLICANT:  Tjoelker, Larry W.
;    APPLICANT:  Wilder, Cheryl L.
;    TITLE OF INVENTION:  Platelet-Activating Factor
;    TITLE OF INVENTION:  Acetylhydrolase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,232
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/318,905
;      FILING DATE:  06-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/133,803
;      FILING DATE:  06-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5656431and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27866/32689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3658
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1876 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  468..1734
US-08-483-232-24

  Query Match             76.0%;  Score 15.2;  DB 1;  Length 1876;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||||||||| ||  |||
Db     432 CCCCGCCGTGGGACCTTCTG 451


RESULT 10
US-08-485-938A-24
; Sequence 24, Application US/08485938A
; Patent No. 5847088
;  GENERAL INFORMATION:
;    APPLICANT:  Cousens, Lawrence S.
;    APPLICANT:  Eberhardt, Christine D.
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Le Trong, Hai
;    APPLICANT:  Tjoelker, Larry W.
;    APPLICANT:  Wilder, Cheryl L.
;    TITLE OF INVENTION:  Platelet-Activating Factor
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;    TITLE OF INVENTION:  Acetylhydrolase
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,938A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/318,905
;      FILING DATE:  06-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/133,803
;      FILING DATE:  06-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5847088and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27866/32792
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3658
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1876 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  468..1734
US-08-485-938A-24

  Query Match             76.0%;  Score 15.2;  DB 2;  Length 1876;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCCTGGGTCCGCCTG 20
           ||||||||||||  ||  |||
Db     432 CCCCGCCGTGGGACCTTCTG 451


RESULT 11
US-08-910-041-24
; Sequence 24, Application US/08910041
; Patent No. 5977308
;  GENERAL INFORMATION:
;    APPLICANT:  Cousens, Lawrence S.
;    APPLICANT:  Eberhardt, Christine D.
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Le Trong, Hai
;    APPLICANT:  Tjoelker, Larry W.
;    APPLICANT:  Wilder, Cheryl L.
;    TITLE OF INVENTION:  Platelet-Activating Factor
;    TITLE OF INVENTION:  Acetylhydrolase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,041
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/483,232
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/318,905
;      FILING DATE:  06-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/133,803
;      FILING DATE:  06-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  27866/34026
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3658
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1876 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  468..1734
US-08-910-041-24

  Query Match             76.0%;  Score 15.2;  DB 2;  Length 1876;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           ||||||||||||  ||  |||
Db     432 CCCCGCCGTGGGACCTTCTG 451


RESULT 12
US-09-328-474-24
; Sequence 24, Application US/09328474
; Patent No. 6045794
;  GENERAL INFORMATION:
;    APPLICANT:  Cousens, Lawrence S.
;    APPLICANT:  Eberhardt, Christine D.
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Le Trong, Hai
;    APPLICANT:  Tjoelker, Larry W.
;    APPLICANT:  Wilder, Cheryl L.
;    TITLE OF INVENTION:  Platelet-Activating Factor
;    TITLE OF INVENTION:  Acetylhydrolase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/328,474
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/483,232
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/318,905
;      FILING DATE:  06-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/133,803
;      FILING DATE:  06-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  27866/34026
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3658
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1876 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  468..1734
US-09-328-474-24

  Query Match             76.0%;  Score 15.2;  DB 3;  Length 1876;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           ||||||||||||  ||  |||
Db     432 CCCCGCCGTGGGACCTTCTG 451


RESULT 13
US-09-100-546-24
; Sequence 24, Application US/09100546
; Patent No. 6099836
;  GENERAL INFORMATION:
;    APPLICANT:  Cousens, Lawrence S.
;    APPLICANT:  Eberhardt, Christine D.
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Le Trong, Hai
;    APPLICANT:  Tjoelker, Larry W.
;    APPLICANT:  Wilder, Cheryl L.
;    TITLE OF INVENTION:  Platelet-Activating Factor
;    TITLE OF INVENTION:  Acetylhydrolase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,546
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/010,715
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/318,905
;      FILING DATE:  06-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/133,803
;      FILING DATE:  06-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6099836and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27866/32793
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3658
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1876 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  468..1734
US-09-100-546-24

  Query Match             76.0%;  Score 15.2;  DB 3;  Length 1876;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           ||||||||||||  ||  |||
Db     432 CCCCGCCGTGGGACCTTCTG 451


RESULT 14
US-09-010-715-24
; Sequence 24, Application US/09010715
; Patent No. 6146625
;  GENERAL INFORMATION:
;    APPLICANT:  Cousens, Lawrence S.
;    APPLICANT:  Eberhardt, Christine D.
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Le Trong, Hai
;    APPLICANT:  Tjoelker, Larry W.
;    APPLICANT:  Wilder, Cheryl L.
;    TITLE OF INVENTION:  Platelet-Activating Factor
;    TITLE OF INVENTION:  Acetylhydrolase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/010,715
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/318,905
;      FILING DATE:  06-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/133,803
;      FILING DATE:  06-OCT-1993
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6146625and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27866/32793
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3658
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1876 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  468..1734
US-09-010-715-24

  Query Match             76.0%;  Score 15.2;  DB 3;  Length 1876;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           ||||||||||||  ||  |||
Db     432 CCCCGCCGTGGGACCTTCTG 451


RESULT 15
US-09-577-758-24
; Sequence 24, Application US/09577758
; Patent No. 6203790
;  GENERAL INFORMATION:
;    APPLICANT:  Cousens, Lawrence S.
;    APPLICANT:  Eberhardt, Christine D.
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Le Trong, Hai
;    APPLICANT:  Tjoelker, Larry W.
;    APPLICANT:  Wilder, Cheryl L.
;    TITLE OF INVENTION:  Platelet-Activating Factor
;    TITLE OF INVENTION:  Acetylhydrolase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/577,758
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/010,715
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/133,803
;      FILING DATE:  06-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6203790and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27866/32793
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3658
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1876 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  468..1734
US-09-577-758-24

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 1876;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           ||||||||||||  ||  |||
Db     432 CCCCGCCGTGGGACCTTCTG 451


Search completed:  November  2, 2002, 16:50:59
Job time :  19.5455 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 16:08:01 ; Search time 719.455 Seconds
(without alignments)
375.200 Million cell updates/sec

Title: US-09-856-803-8
Perfect score: 20
Sequence: 1 ccccgccgtgggtccgcctg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
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12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
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3		20	100.0	848	10	BI767868	BI767868 603060993
4		20	100.0	853	10	BI915042	BI915042 603177231
5		20	100.0	885	10	BI820274	BI820274 603036831
6		20	100.0	950	9	AL553611	AL553611 AL553611
7		18.4	92.0	406	10	BE245562	BE245562 TCBAP1E21
8		18.4	92.0	646	10	BI911023	BI911023 603068746
9	c	17.4	87.0	839	12	CNS04A9U	AL281595 Tetraodon
10		17.4	87.0	871	12	CNS02X3Y	AL217879 Tetraodon
11		17.4	87.0	887	12	CNS02BGT	AL189830 Tetraodon
12	c	17.4	87.0	1481	10	BM463935	BM463935 AGENCOURT
13	c	16.8	84.0	336	9	BB870361	BB870361 BB870361
14	c	16.8	84.0	339	9	BB868580	BB868580 BB868580
15	c	16.8	84.0	352	9	BB871963	BB871963 BB871963
16	c	16.8	84.0	406	9	BB850291	BB850291 BB850291
17	c	16.8	84.0	408	9	AA023897	AA023897 mh94f02.r
18	c	16.8	84.0	428	9	BB849807	BB849807 BB849807
19	c	16.8	84.0	436	9	BB850773	BB850773 BB850773
20	c	16.8	84.0	437	9	BB859092	BB859092 BB859092
21	c	16.8	84.0	465	9	AI187261	AI187261 qe40d01.s
22	c	16.8	84.0	475	10	BF099718	BF099718 601751355
23		16.8	84.0	488	9	AW940657	AW940657 GH17420.3
24	c	16.8	84.0	516	9	BB857075	BB857075 BB857075
25	c	16.8	84.0	561	10	BI660051	BI660051 603302772
26	c	16.8	84.0	589	9	BB633967	BB633967 BB633967
27		16.8	84.0	605	10	BE302495	BE302495 ba66d06.y
28	c	16.8	84.0	656	9	BB664934	BB664934 BB664934
29	c	16.8	84.0	702	10	BI648708	BI648708 603277024
30		16.8	84.0	737	10	BF631191	BF631191 HVSMEb001
31	c	16.8	84.0	745	11	AK006219	AK006219 Mus muscu
32	c	16.8	84.0	746	10	BI653538	BI653538 603300550
33	c	16.8	84.0	751	10	BI854786	BI854786 6033B1745
34	c	16.8	84.0	768	10	BE570011	BE570011 601332033
35	c	16.8	84.0	779	12	CNS021QC	AL177213 Tetraodon
36		16.8	84.0	781	12	CNS03G9F	AL242700 Tetraodon
37		16.8	84.0	784	10	BG365241	BG365241 HVSMEi000
38	c	16.8	84.0	797	10	BI691700	BI691700 603307394
39	c	16.8	84.0	804	10	BI686272	BI686272 603312780
40	c	16.8	84.0	829	9	AL530570	AL530570 AL530570
41		16.8	84.0	857	10	BF256721	BF256721 HVSMEf001
42		16.8	84.0	869	12	BH255582	BH255582 LDH10MCR2
43	c	16.8	84.0	873	10	BG539046	BG539046 602568415
44	c	16.8	84.0	883	10	BF244543	BF244543 601862850
45	c	16.8	84.0	925	10	BI146262	BI146262 602911092

ALIGNMENTS

RESULT 1
AV647785
LOCUS AV647785 427 bp mRNA linear EST 15-JAN-2002
DEFINITION AV647785 GLC Homo sapiens cDNA clone GLCBCA03 3', mRNA sequence.
ACCESSION AV647785
VERSION AV647785.1 GI:9868799
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 427)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES Location/Qualifiers
source 1..427
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCBCA03"
/clone_lib="GLC"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

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BASE COUNT       80 a    149 c    127 g     71 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 427;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||||||||
Db    132 CCCCGCCGTGGGTCCGCCTG 151


RESULT 2
BI907636
LOCUS       BI907636                659 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603065545F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214802 5',
            mRNA sequence.
ACCESSION   BI907636
VERSION     BI907636.1  GI:16170473
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 659)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11539  row: i  column: 11
            High quality sequence stop: 655.
FEATURES             Location/Qualifiers
     source          1. .659
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5214802"
                     /clone_lib="NIH_MGC_118"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
BASE COUNT      127 a    198 c    194 g    140 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 10;  Length 659;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||||||||
Db    114 CCCCGCCGTGGGTCCGCCTG 133


RESULT 3
BI767868
LOCUS       BI767868                848 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603060993F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5210231 5',
            mRNA sequence.
ACCESSION   BI767868
VERSION     BI767868.1  GI:15759446
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11527  row: j  column: 24
            High quality sequence stop: 845.
FEATURES             Location/Qualifiers
     source          1. .848
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5210231"
                     /clone_lib="NIH_MGC_122"
                     /lab_host="DH10B"
                     /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
                     anonymous pool of 24 week female lung, 16 week female
                     spleen, and 20-22 week male spleens.  Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon  cloning).  Average insert size 1.4 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was  constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking  code 026. Note:
                     this is a NIH_MGC Library."
BASE COUNT      157 a    265 c    230 g    195 t      1 others
ORIGIN

  Query Match             100.0%;  Score 20;  DB 10;  Length 848;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||||||||
Db    137 CCCCGCCGTGGGTCCGCCTG 156


RESULT 4
BI915042
LOCUS       BI915042                853 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603177231F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5241774 5',
            mRNA sequence.
ACCESSION   BI915042
VERSION     BI915042.1  GI:16179135
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11609 row: m column: 07
High quality sequence stop: 840.

FEATURES Location/Qualifiers
source 1. .853
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5241774"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

BASE COUNT 161 a 269 c 229 g 194 t
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 853;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCTG 20
||||||||||||||||||||
Db 125 CCCCGCCGTGGGTCCGCCTG 144

RESULT 5
BI820274
LOCUS BI820274 885 bp mRNA linear EST 04-OCT-2001
DEFINITION 603036831F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178031 5', mRNA sequence.
ACCESSION BI820274
VERSION BI820274.1 GI:15931824
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 885)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11443 row: m column: 08
High quality sequence stop: 839.

FEATURES Location/Qualifiers
source 1. .885
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5178031"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

BASE COUNT 172 a 263 c 245 g 205 t
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 885;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCTG 20
||||||||||||||||||||
Db 132 CCCCGCCGTGGGTCCGCCTG 151

RESULT 6
AL553611
LOCUS AL553611 950 bp mRNA linear EST 16-FEB-2001
DEFINITION AL553611 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI078YB15 5 prime, mRNA sequence.
ACCESSION AL553611
VERSION AL553611.1 GI:12893606
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 950)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES Location/Qualifiers
source 1. .950
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI078YB15"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 183 a 291 c 262 g 210 t 4 others
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 950;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCTG 20
||||||||||||||||||||
Db 112 CCCCGCCGTGGGTCCGCCTG 131

RESULT 7
BE245562
LOCUS BE245562 406 bp mRNA linear EST 03-OCT-2001
DEFINITION TCBAP1E2132 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2132, mRNA sequence.
ACCESSION BE245562

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VERSION     BE245562.1  GI:9097308
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 406)
  AUTHORS   Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D.
            , Bouck,J., Gibbs,R.A. and Margolin,J.F.
  TITLE     Pediatric Leukemia cDNA Sequencing Project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Dr. Judith F. Margolin
            Texas Children's Cancer Center and Human Genome Sequencing Center
            at Baylor College of Medicine
            1102 Bates, MC3-3320 Houston, TX 77030, USA
            Tel: 832-824-4536
            Fax: 832-825-4038
            Email: clones@txccc.org
            Citation: Carninci,P. and Hayashizaki,Y. High efficiency
            full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
            Seq primer: M13 primer.
FEATURES             Location/Qualifiers
     source          1. .406
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="TCBAP2132"
                     /clone_lib="Pediatric pre-B cell acute lymphoblastic
                     leukemia Baylor-HGSC project=TCBA"
                     /sex="male"
                     /tissue_type="leukopheresis"
                     /cell_type="pre-B cell"
                     /dev_stage="pediatric 2 years"
                     /lab_host="DH10B"
                     /note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
                     First strand cDNA was primed with an anchored
                     XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCCGCAGGAGGAG(T)VN
                     3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand
                     was primed with a BamH1-dC primer
                     [5'AGAGAGCTCGGATCCGCGGCCGCAATAATAATAAT(C) 3'].
                     Double-stranded cDNA was then digested with BamHl and XhoI
                     and directionally cloned into the BamH1 and SalI sites of
                     lambda pSB vector. Library went through one round of
                     normalization. Library was constructed by Wei Yu at RIKEN
                     of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
                     Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M,
                     Schneider C, Hayashizaki Y, High efficiency selection of
                     full-length cDNA by improved biotinylated cap trapper.,
                     DNA Res 4: 1, 61-6, Feb 28, 1997)"
BASE COUNT       73 a    140 c    130 g     61 t      2 others
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 10;  Length 406;
  Best Local Similarity  95.0%;  Pred. No. 8.7e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||||||||||||||| |
Db     158 CCCCGCCGTGGGTCCGCCCG 177


RESULT 8
BI911023
LOCUS       BI911023                 646 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603068746F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217922 5',
            mRNA sequence.
ACCESSION   BI911023
VERSION     BI911023.1  GI:16174544
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11547  row: k  column: 11
            High quality sequence stop: 643.
FEATURES             Location/Qualifiers
     source          1. .646
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5217922"
                     /clone_lib="NIH_MGC_118"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
BASE COUNT      114 a    209 c    189 g    134 t
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 10;  Length 646;
  Best Local Similarity  95.0%;  Pred. No. 8.7e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||||||||||||||| |
Db     126 CCCCGCCGTGGGTCCGCCCG 145


RESULT 9
CNS04A9U/c
LOCUS       CNS04A9U                 839 bp    DNA     linear   GSS 21-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            095I07 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL281595
VERSION     AL281595.1  GI:8019918
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 839)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 839)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 839)
```

```
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .839
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="095I07"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG095AE04SP1-end :
                     PUC-Ori"
BASE COUNT      165 a    250 c    251 g    169 t      4 others
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 12;  Length 839;
  Best Local Similarity   94.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||| |||
Db    657 CCCGCCGTGGGTCCGGCTG 639


RESULT 10
CNS02X3Y
LOCUS       CNS02X3Y                871 bp    DNA     linear   GSS 15-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            177L08 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL217879
VERSION     AL217879.1  GI:7876698
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 871)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 871)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="177L08"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG177DF04SP1-end :
                     PUC-Ori"
BASE COUNT      177 a    257 c    258 g    177 t      2 others
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 12;  Length 871;
  Best Local Similarity   94.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||| |||
Db    180 CCCGCCGTGGGTCCGGCTG 198


RESULT 11
CNS02BGT
LOCUS       CNS02BGT                887 bp    DNA     linear   GSS 12-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            253B21 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL189830
VERSION     AL189830.1  GI:7827934
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 887)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 887)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 887)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .887
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="253B21"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG253CA11LP1-end : T7"
BASE COUNT      181 a    255 c    262 g    185 t      4 others
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 12;  Length 887;
  Best Local Similarity   94.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||| |||
Db    315 CCCGCCGTGGGTCCGGCTG 333


RESULT 12
BM463935/c
LOCUS       BM463935                1481 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6445415 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5539947
            5', mRNA sequence.
ACCESSION   BM463935
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VERSION     BM463935.1  GI:18512977
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1481)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12235  row: e  column: 04
            High quality sequence start: 88
            High quality sequence stop: 451.
FEATURES             Location/Qualifiers
     source          1. .1481
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5539947"
                     /clone_lib="NIH_MGC_72"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      261 a    602 c    334 g    283 t      1 others
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 10;  Length 1481;
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  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCCGCCGTGGGTCCGCCTG 20
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Db      50 CCCGCCGTGGGTCCGCCCG 32


RESULT 13
BB870361/c
LOCUS       BB870361                336 bp    mRNA    linear   EST 27-NOV-2001
DEFINITION  BB870361 RIKFN full-length enriched, 14 days embryo lung Mus
            musculus cDNA clone G630020K24 5', mRNA sequence.
ACCESSION   BB870361
VERSION     BB870361.1  GI:17116571
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 336)
  AUTHORS   Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
            Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
            ,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
            Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
            , Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
            Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
            ,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.
            , Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
            2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .336
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G630020K24"
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                     /tissue_type="lung"
                     /dev_stage="14 days embryo"
BASE COUNT       67 a    109 c    102 g     58 t
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 9;  Length 336;
  Best Local Similarity   90.0%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||||| ||||||| |||
Db      59 CCCCGCCGGGGGTCCGGCTG 40


RESULT 14
BB868580/c
LOCUS       BB868580                339 bp    mRNA    linear   EST 27-NOV-2001
DEFINITION  BB868580 RIKEN full-length enriched, 0 day neonate cortex Mus
            musculus cDNA clone G630006G17 5', mRNA sequence.
ACCESSION   BB868580
VERSION     BB868580.1  GI:17114790
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 339)
  AUTHORS   Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
            Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
            ,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
            Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
            , Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
            Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
            ,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.
            , Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
            2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
```

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara ,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

```
FEATURES             Location/Qualifiers
     source          1. .339
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G630006G17"
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                     cortex"
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ORIGIN

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  Best Local Similarity   90.0%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          |||||||| ||||||| |||
Db    115 CCCCGCCGGGGGTCCGGCTG 96


RESULT 15
BB871963/c
LOCUS       BB871963                352 bp    mRNA    linear   EST 27-NOV-2001
DEFINITION  BB871963 RIKEN full-length enriched, 14 days embryo lung Mus
            musculus cDNA clone G630033L09 5', mRNA sequence.
ACCESSION   BB871963
VERSION     BB871963.1  GI:17118173
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 352)
  AUTHORS   Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
            Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
            ,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
            Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
            , Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
            Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
            ,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.
            , Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
            2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
            wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
            Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
            e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .352
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G630033L09"
                     /clone_lib="RIKEN full-length enriched, 14 days embryo
                     lung"
                     /tissue_type="lung"
                     /dev_stage="14 days embryo"
BASE COUNT       74 a    111 c    106 g     61 t
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 9;  Length 352;
  Best Local Similarity   90.0%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          |||||||| ||||||| |||
Db     59 CCCCGCCGGGGGTCCGGCTG 40


Search completed: November  2, 2002, 17:57:18
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GenCore version 5.1.3

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264.899 Million cell updates/sec

Title: US-09-856-803-9
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Sequence: 1 ggctgggggcgcctcagcgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	230	4	US-09-437-457-8	Sequence 8, Appli
	2	15.8	79.0	6816	4	US-09-404-650-1	Sequence 1, Appli
	3	15.8	79.0	6855	4	US-09-404-650-3	Sequence 3, Appli
	4	15.8	79.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	5	15.8	79.0	4411529	4	US-09-103-840A-1	Sequence 1, Appli
c	6	15.2	76.0	420	4	US-08-943-731-198	Sequence 198, App
	7	15.2	76.0	654	1	US-08-390-858B-8	Sequence 8, Appli
c	8	15.2	76.0	1926	2	US-08-978-182-2	Sequence 2, Appli
c	9	15.2	76.0	1926	2	US-09-205-681-2	Sequence 2, Appli
	10	15.2	76.0	2370	1	US-08-104-072B-7	Sequence 7, Appli
	11	15.2	76.0	2370	1	US-08-351-413-8	Sequence 8, Appli
	12	15.2	76.0	2370	2	US-09-025-583-8	Sequence 8, Appli
c	13	15.2	76.0	2793	2	US-08-795-868-13	Sequence 13, Appl
c	14	15.2	76.0	2793	4	US-09-303-069-13	Sequence 13, Appl
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c	16	15.2	76.0	3032	4	US-09-546-238-1	Sequence 1, Appli
	17	15.2	76.0	11459	4	US-09-454-721A-3	Sequence 3, Appli
c	18	15.2	76.0	20084	4	US-08-943-731-5	Sequence 5, Appli
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c	21	14.8	74.0	2186	4	US-09-184-001-1	Sequence 1, Appli
	22	14.8	74.0	2421	1	US-08-063-552-1	Sequence 1, Appli
	23	14.8	74.0	2421	5	PCT-US93-05704-1	Sequence 1, Appli
	24	14.8	74.0	3271	2	US-08-852-806-1	Sequence 1, Appli
	25	14.8	74.0	3271	3	US-09-163-669-1	Sequence 1, Appli
	26	14.8	74.0	35060	3	US-08-814-095-7	Sequence 7, Appli
	27	14.4	72.0	803	1	US-08-390-858B-37	Sequence 37, Appl
	28	14.2	71.0	60	1	US-08-219-012-82	Sequence 82, Appl
	29	14.2	71.0	60	4	US-08-687-421-270	Sequence 270, App
	30	14.2	71.0	256	4	US-09-060-756-699	Sequence 699, App
	31	14.2	71.0	333	4	US-09-060-756-233	Sequence 233, App
c	32	14.2	71.0	454	2	US-08-474-379C-21	Sequence 21, Appl
c	33	14.2	71.0	688	5	PCT-US94-04361-26	Sequence 26, Appl
	34	14.2	71.0	1026	4	US-07-751-891B-24	Sequence 24, Appl
	35	14.2	71.0	1028	4	US-08-118-200-1	Sequence 1, Appli
	36	14.2	71.0	1028	4	US-08-458-745-1	Sequence 1, Appli
	37	14.2	71.0	1098	2	US-08-948-616-6	Sequence 6, Appli
	38	14.2	71.0	1098	2	US-09-193-510-6	Sequence 6, Appli
	39	14.2	71.0	1098	4	US-09-368-402-6	Sequence 6, Appli
c	40	14.2	71.0	1318	4	US-09-008-271A-20	Sequence 20, Appl
	41	14.2	71.0	1351	4	US-08-697-954-3	Sequence 3, Appli
c	42	14.2	71.0	1553	4	US-09-217-490-1	Sequence 1, Appli
c	43	14.2	71.0	1642	1	US-08-723-938-2	Sequence 2, Appli
c	44	14.2	71.0	1642	2	US-09-080-538-2	Sequence 2, Appli
	45	14.2	71.0	1844	2	US-08-538-816A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-437-457-8/c
; Sequence 8, Application US/09437457
; Patent No. 6273893
; GENERAL INFORMATION:
; APPLICANT: Giordano, Anthony
; APPLICANT: Xavier, Ashish
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
; TITLE OF INVENTION: INTERACTIONS AND MRNA FUNCTIONALITY
; FILE REFERENCE: 50093/014001
; CURRENT APPLICATION NUMBER: US/09/437,457
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-437-457-8

Query Match 100.0%; Score 20; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GGCTGGGGGCGCCTCAGCGG 20
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Db    191 GGCTGGGGGCGCCTCAGCGG 172
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RESULT 2
US-09-404-650-1
; Sequence 1, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

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;   LOCATION: (192)..(6716)
US-09-404-650-1

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 6816;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCG 19
          ||||| |||||| |||||||
Db   6283 GGCTGCGGGCGCATCAGCG 6301


RESULT 3
US-09-404-650-3
; Sequence 3, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
;  APPLICANT: Dietrich, Paul S.
;  APPLICANT: McGivern, Joseph G.
;  TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
;  TITLE OF INVENTION: AND USES
;  FILE REFERENCE: R0043B-REG sequence listing
;  CURRENT APPLICATION NUMBER: US/09/404,650
;  CURRENT FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 6855
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (192)..(6755)
US-09-404-650-3

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 6855;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCG 19
          ||||| |||||| |||||||
Db   6322 GGCTGCGGGCGCATCAGCG 6340


RESULT 4
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 4403765;
  Best Local Similarity   89.5%;  Pred. No. 42;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCG 19
          ||||||| ||| ||||||
Db 3667270 GGCTGGGGTCGCTTCAGCG 3667288


RESULT 5
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 4411529;
  Best Local Similarity   89.5%;  Pred. No. 42;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCG 19
          ||||||| ||| ||||||
Db 3672484 GGCTGGGGTCGCTTCAGCG 3672502


RESULT 6
US-08-943-731-198/c
; Sequence 198, Application US/08943731
; Patent No. 6265157
;  GENERAL INFORMATION:
;    APPLICANT:  PROCKOP, DARWIN J.
;    APPLICANT:  SPOTILA, LORETTA D.
;    APPLICANT:  DELTAS, CONSTANTINOS D.
;    APPLICANT:  SEREDA, LARISA
;    APPLICANT:  LARSON, ANDREA W.
;    APPLICANT:  PACK, MICHAEL
;    APPLICANT:  COLIGE, ALAIN
;    APPLICANT:  EARLY, JAMES
;    APPLICANT:  KORKKO, JARMO
;    APPLICANT:  ALA-KOKKO, LEENA, et al.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR DETECTING
;    TITLE OF INVENTION:  ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
;    NUMBER OF SEQUENCES:  666
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PANITCH SCHWARZE JACOBS & NADEL, P.C.
;      STREET:  ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
;      STREET:  FLR.
;      CITY:  PHILADELPHIA
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103-7086
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,731
;      FILING DATE:  03-OCT-1997
;      CLASSIFICATION:  435
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/212,322
;      FILING DATE:  14-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/803,628
;      FILING DATE:  03-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DOYLE LEARY Ph.D., KATHRYN
;      REGISTRATION NUMBER:  36,317
;      REFERENCE/DOCKET NUMBER:  9598-27
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-965-1284
;      TELEFAX:  215-567-2991
;      TELEX:  831-494
;  INFORMATION FOR SEQ ID NO:  198:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  420 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-943-731-198

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 420;
  Best Local Similarity   85.0%;  Pred. No. 2.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           |||||||||||  || || ||
Db      82 GGCTGGGGGCGTCTGAGAGG 63


RESULT 7
US-08-390-858B-8
; Sequence 8, Application US/08390858B
; Patent No. 5643727
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John C.
;    APPLICANT:  Harigai, Masayoshi
;    TITLE OF INVENTION:  Bcl-2 Gene Inhibitory Element Binding
;    TITLE OF INVENTION:  Factor
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,858B
;      FILING DATE:  16-FEB-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1366
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  654 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..652
US-08-390-858B-8

  Query Match             76.0%;  Score 15.2;  DB 1;  Length 654;
  Best Local Similarity   85.0%;  Pred. No. 2.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           |||||||||||  | ||||
Db      16 GGCTGGGGGCGCGACCGCGG 35


RESULT 8
US-08-978-182-2/c
; Sequence 2, Application US/08978182
; Patent No. 5849556
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Yue, Henry
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Kaser, Matthew
;    APPLICANT:  Mathur, Preete
;    TITLE OF INVENTION:  HUMAN GROWTH-RELATED CDC10 HOMOLOG
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,182
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0426 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1926 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  TLYMNOT06
;      CLONE:  3003826
US-08-978-182-2

  Query Match             76.0%;  Score 15.2;  DB 2;  Length 1926;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||| | ||||||||||| |
Db     261 GGCGGTGGGCGCCTCAGCAG 242


RESULT 9
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US-09-205-681-2/c
; Sequence 2, Application US/09205681
; Patent No. 5952214
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Yue, Henry
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Kaser, Matthew
;    APPLICANT:  Mathur, Preete
;    TITLE OF INVENTION:  HUMAN GROWTH-RELATED CDC10 HOMOLOG
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/205,681
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/978,182
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0426 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1926 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  TLYMNOT06
;      CLONE:  3003826
US-09-205-681-2

  Query Match             76.0%;  Score 15.2;  DB 2;  Length 1926;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||| | |||||||||||| |
Db     261 GGCGGTGGGCGCCTCAGCAG 242


RESULT 10
US-08-104-072B-7
; Sequence 7, Application US/08104072B
; Patent No. 5639948
;  GENERAL INFORMATION:
;    APPLICANT:  Michiels, Frank
;    APPLICANT:  Morioka, Sinji
;    APPLICANT:  Scheirlinck, Trees
;    APPLICANT:  Komari, Tosihiko
;    TITLE OF INVENTION:  Stamen-specific Promoters from Rice
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  3100 No. 5639948west Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/104,072B
;      FILING DATE:  05-AUG-1993
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO 9200272
;      FILING DATE:  06-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 91403352.7
;      FILING DATE:  10-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 91402590.3
;      FILING DATE:  27-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 91400318.1
;      FILING DATE:  08-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kowalchyk, Katherine M.
;      REGISTRATION NUMBER:  36,848
;      REFERENCE/DOCKET NUMBER:  8076.93USWO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2370 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Oryza sativa
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  1..1808
;      OTHER INFORMATION:  /function= "anther specific PT42
;      OTHER INFORMATION:  promoter"
;    FEATURE:
;      NAME/KEY:  TATA_signal
;      LOCATION:  1748..1755
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1780
;      OTHER INFORMATION:  /product= "transcription
;      OTHER INFORMATION:  initiation"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1809
;      OTHER INFORMATION:  /product= "ATG start translation
;      OTHER INFORMATION:  T42"
US-08-104-072B-7

  Query Match             76.0%;  Score 15.2;  DB 1;  Length 2370;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||| |||||||| || ||||
Db    1874 GGCGGGGGGCGCGTCGGCGG 1893


RESULT 11
US-08-351-413-8
; Sequence 8, Application US/08351413
; Patent No. 5750867
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;  GENERAL INFORMATION:
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Leemans, Jan
;    TITLE OF INVENTION:  Maintenance of male-sterile plants
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH & BIRCH
;      STREET:  8110 Gatehouse Road, Suite 500 East
;      CITY:  Falls Church
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  2046
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/351,413
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/899,072
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/970,849
;      FILING DATE:  03-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svensson, Leonard R.
;      REGISTRATION NUMBER:  30,330
;      REFERENCE/DOCKET NUMBER:  2121-102PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2370 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Oryza sativa
;      STRAIN:  Akihikari
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..1808
;      OTHER INFORMATION:  /label= PT42
;      OTHER INFORMATION:  /note= "sequence comprising anther specific
;      OTHER INFORMATION:  promoter PT42"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1748..1755
;      OTHER INFORMATION:  /label= TATA
;      OTHER INFORMATION:  /note= "TATA Box"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1780
;      OTHER INFORMATION:  /note= "transcription initiation
;      OTHER INFORMATION:  site determined by primer extension"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1809
;      OTHER INFORMATION:  /label= ATG
;      OTHER INFORMATION:  /note= "ATG start of translation of rice T42 gene"
US-08-351-413-8

  Query Match             76.0%;  Score 15.2;  DB 1;  Length 2370;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||| ||||||||| || ||||
Db    1874 GGCGGGGGGCGCGTCGGCGG 1893


RESULT 12
US-09-025-583-8
; Sequence 8, Application US/09025583
; Patent No. 5977433
;  GENERAL INFORMATION:
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Leemans, Jan
;    TITLE OF INVENTION:  Maintenance of male-sterile plants
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH & BIRCH
;      STREET:  8110 Gatehouse Road, Suite 500 East
;      CITY:  Falls Church
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  2046
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,583
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/351,413
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/899,072
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/970,849
;      FILING DATE:  03-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svensson, Leonard R.
;      REGISTRATION NUMBER:  30,330
;      REFERENCE/DOCKET NUMBER:  2121-102PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2370 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Oryza sativa
;      STRAIN:  Akihikari
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..1808
;      OTHER INFORMATION:  /label= PT42
;      OTHER INFORMATION:  /note= "sequence comprising anther specific
;      OTHER INFORMATION:  promoter PT42"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1748..1755
;      OTHER INFORMATION:  /label= TATA
;      OTHER INFORMATION:  /note= "TATA Box"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1780
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;      OTHER INFORMATION:  /note= "transcription initiation
;      OTHER INFORMATION:  site determined by primer extension"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1809
;      OTHER INFORMATION:  /label= ATG
;      OTHER INFORMATION:  /note= "ATG start of translation of rice T42 gene"
US-09-025-583-8

  Query Match            76.0%;  Score 15.2;  DB 2;  Length 2370;
  Best Local Similarity  85.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||| |||||||| || ||||
Db    1874 GGCGGGGGGCGCGTCGGCGG 1893


RESULT 13
US-08-795-868-13/c
; Sequence 13, Application US/08795868
; Patent No. 5846773
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Mu-En
;    APPLICANT:  Hsieh, Chung-Ming
;    TITLE OF INVENTION:  A SINGLE GENE ENCODING AORTIC-SPECIFIC
;    TITLE OF INVENTION:  AND STRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,868
;      FILING DATE:  06-FEB-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/494,577
;      FILING DATE:  22-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  05433/032001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2793 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  3...1983
;      OTHER INFORMATION:
US-08-795-868-13

  Query Match            76.0%;  Score 15.2;  DB 2;  Length 2793;
  Best Local Similarity  85.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||| |||| |||| ||||
Db    1170 GGCTGCGGGCCCCTCGGCGG 1151


RESULT 14
US-09-303-069-13/c
; Sequence 13, Application US/09303069A
; Patent No. 6350592
; GENERAL INFORMATION:
;  APPLICANT: Lee, Mu-En
;  APPLICANT: Hsieh, Chung-Ming
;  TITLE OF INVENTION: SINGLE GENE ENCODING AORTIC-SPECIFIC AND STRIATED-SPECIFIC
;  TITLE OF INVENTION: MUSCLE CELL ISOFORMS AND USES THEREOF
;  FILE REFERENCE: 05433/039001
;  CURRENT APPLICATION NUMBER: US/09/303,069A
;  CURRENT FILING DATE: 1999-04-30
;  EARLIER APPLICATION NUMBER: US 09/134,250
;  EARLIER FILING DATE: 1998-08-14
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 2793
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3)...(1985)
US-09-303-069-13

  Query Match            76.0%;  Score 15.2;  DB 4;  Length 2793;
  Best Local Similarity  85.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||| |||| |||| ||||
Db    1170 GGCTCCGGGCCCCTCGGCGG 1151


RESULT 15
US-08-990-140-1/c
; Sequence 1, Application US/08990140A
; Patent No. 6093795
; GENERAL INFORMATION:
;  APPLICANT: Olsen, Henrik S.
;  APPLICANT: Ruben, Steven M.
;  APPLICANT: Sonenberg, Nahum
;  APPLICANT: Methot, Nathalie
;  APPLICANT: Rom, Eran
;  TITLE OF INVENTION: Human Prt1-like Subunit Protein (hPrt1) and Human
;  TITLE OF INVENTION: eIF4GF-like Protein (p97) Genes
;  FILE REFERENCE: 1488.0700001
;  CURRENT APPLICATION NUMBER: US/08/990,140A
;  CURRENT FILING DATE: 1997-12-12
;  EARLIER APPLICATION NUMBER: US 60/033,151
;  EARLIER FILING DATE: 1996-12-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3032
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (97)..(2718)
US-08-990-140-1

  Query Match            76.0%;  Score 15.2;  DB 3;  Length 3032;
  Best Local Similarity  85.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           |||||| |||| ||| ||||
Db     189 GGCTGGCGGCGGCTCGGCGG 170
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Search completed: November 2, 2002, 17:08:37
Job time : 1076.55 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 16:08:01 ; Search time 719.455 Seconds
(without alignments)
375.200 Million cell updates/sec

Title: US-09-856-803-9
Perfect score: 20
Sequence: 1 ggctgggggcgcctcagcgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	406	10	BE245562	BE245562 TCBAP1E21
c 2	20	100.0	646	10	BI911023	BI911023 603068746
c 3	18.4	92.0	240	9	BB386852	BB386852 BB386852
c 4	18.4	92.0	427	9	AV647785	AV647785 AV647785
c 5	18.4	92.0	659	10	BI907636	BI907636 603065545
c 6	18.4	92.0	683	10	BG284879	BG284879 602409113
c 7	18.4	92.0	853	10	BI915042	BI915042 603177231
c 8	18.4	92.0	950	9	AL553611	AL553611 AL553611
c 9	18.4	92.0	995	10	BI519989	BI519989 603071783
c 10	17.4	87.0	568	10	BE337782	BE337782 894048D05
c 11	17.4	87.0	610	10	BI722560	BI722560 1031062G0
c 12	17.4	87.0	642	10	BI527454	BI527454 1024081G0
c 13	17.4	87.0	668	10	BI719349	BI719349 1031042H1
c 14	17.4	87.0	675	10	BG845027	BG845027 1024008E0
c 15	17.4	87.0	684	10	BG845026	BG845026 1024008E0
c 16	17.4	87.0	732	10	BF864370	BF864370 963051B07
c 17	17.4	87.0	766	10	BF866118	BF866118 963066F01
c 18	17	85.0	161	10	C84644	C84644 C84644 oste
c 19	17	85.0	681	10	BI954411	BI954411 HVSMEm001
c 20	16.8	84.0	97	9	AA648867	AA648867 ns37g08.s
c 21	16.8	84.0	190	10	N91498	N91498 za91a11.s1
22	16.8	84.0	226	9	AV362547	AV362547 AV362547
23	16.8	84.0	228	9	BB311008	BB311008 BB311008
c 24	16.8	84.0	234	9	AA724980	AA724980 ai08d08.s
c 25	16.8	84.0	242	9	AA725280	AA725280 ai16f06.s
c 26	16.8	84.0	255	9	AA831285	AA831285 oc60b07.s
c 27	16.8	84.0	280	10	H45279	H45279 yo65h06.s1
c 28	16.8	84.0	281	9	AA399291	AA399291 zt53g01.s
c 29	16.8	84.0	284	10	BF340043	BF340043 602036982
30	16.8	84.0	293	12	AZ769071	AZ769071 1M0569E19
c 31	16.8	84.0	311	9	AI073807	AI073807 oy69c12.x
c 32	16.8	84.0	311	9	AI273229	AI273229 ql45b02.x
c 33	16.8	84.0	314	10	R25414	R25414 yh50g07.s1
c 34	16.8	84.0	324	9	AW297631	AW297631 UI-H-BW0-
c 35	16.8	84.0	328	9	AA992754	AA992754 ot84e09.s
c 36	16.8	84.0	335	9	AI189106	AI189106 qc98e09.x
c 37	16.8	84.0	342	10	BI035865	BI035865 IL5-NT022
38	16.8	84.0	348	10	R55199	R55199 yj76d09.r1
c 39	16.8	84.0	350	10	R28179	R28179 yh65f09.s1
40	16.8	84.0	355	9	AA577199	AA577199 nm87c01.s
c 41	16.8	84.0	361	10	H28433	H28433 yo54c05.s1
c 42	16.8	84.0	363	10	H21861	H21861 yn78g11.s1
43	16.8	84.0	364	9	AA037568	AA037568 zk34b01.r
c 44	16.8	84.0	365	9	AI209019	AI209019 qg17g11.x
45	16.8	84.0	367	9	AI916036	AI916036 wi44c02.x

ALIGNMENTS

RESULT 1
BE245562/c
LOCUS BE245562 406 bp mRNA linear EST 03-OCT-2001
DEFINITION TCBAP1E2132 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2132, mRNA sequence.
ACCESSION BE245562
VERSION BE245562.1 GI:9097308
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 406)
AUTHORS Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
TITLE Pediatric Leukemia cDNA Sequencing Project
JOURNAL Unpublished (2000)
COMMENT Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@txccc.org
Citation: Carninci,P. and Hayashizaki,Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer.
FEATURES Location/Qualifiers
source 1. .406
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCBAP2132"
/clone_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"

/note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCCGCAGGAGGAG(T)VN 3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand was primed with a BamH1-dC primer [5'AGAGAGCTCGGATCCGCGGCCGCAATAATAATAAT(C) 3']. Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"

BASE COUNT 73 a 140 c 130 g 61 t 2 others
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 406;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGGGCGCCTCAGCGG 20
||||||||||||||||||||
Db 194 GGCTGGGGGCGCCTCAGCGG 175

RESULT 2
BI911023/c
LOCUS BI911023 646 bp mRNA linear EST 16-OCT-2001
DEFINITION 603068746F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217922 5', mRNA sequence.
ACCESSION BI911023
VERSION BI911023.1 GI:16174544
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 646)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11547 row: k column: 11
High quality sequence stop: 643.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5217922"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

BASE COUNT 114 a 209 c 189 g 134 t
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 646;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGGGCGCCTCAGCGG 20
||||||||||||||||||||
Db 162 GGCTGGGGGCGCCTCAGCGG 143

RESULT 3
BB386852/c
LOCUS BB386852 240 bp mRNA linear EST 13-JUL-2000
DEFINITION BB386852 RIKEN full-length enriched, 0 day neonate cerebellum Mus musculus cDNA clone C230048L24 3', mRNA sequence.
ACCESSION BB386852
VERSION BB386852.1 GI:9109663
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 240)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .240
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="C230048L24"
/clone_lib="RIKEN full-length enriched, 0 day neonate cerebellum"
/tissue_type="cerebellum"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 479.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

```
BASE COUNT       59 a     77 c     49 g     55 t
ORIGIN

  Query Match           92.0%;  Score 18.4;  DB 9;  Length 240;
  Best Local Similarity  95.0%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCGG 20
          |||||||||||||||||| ||
Db     29 GGCTGGGGGCGCCTCAGTGG 10
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```
RESULT 4
AV647785/c
LOCUS       AV647785                427 bp    mRNA    linear   EST 15-JAN-2002
DEFINITION  AV647785 GLC Homo sapiens cDNA clone GLCBCA03 3', mRNA sequence.
ACCESSION   AV647785
VERSION     AV647785.1  GI:9868799
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 427)
  AUTHORS   Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
            Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
            Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
            Hu,G., Gu,J., Chen,Z. and Han,Z.
  TITLE     Insight into hepatocellular carcinogenesis at transcriptome level
            by comparing gene expression profiles of hepatocellular carcinoma
            with those of corresponding noncancerous liver
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
  MEDLINE   21625106
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="GLC"
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                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       80 a    149 c    127 g     71 t
ORIGIN

  Query Match           92.0%;  Score 18.4;  DB 9;  Length 427;
  Best Local Similarity  95.0%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCGG 20
          |||||||||||||||||| |
Db    168 GGCTGGGGGCGCCTCAGCAG 149
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```
RESULT 5
BI907636/c
LOCUS       BI907636                659 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603065545F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214802 5',
            mRNA sequence.
ACCESSION   BI907636
VERSION     BI907636.1  GI:16170473
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 659)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11539  row: i  column: 11
            High quality sequence stop: 655.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5214802"
                     /clone_lib="NIH_MGC_118"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
BASE COUNT      127 a    198 c    194 g    140 t
ORIGIN

  Query Match           92.0%;  Score 18.4;  DB 10;  Length 659;
  Best Local Similarity  95.0%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCGG 20
          |||||||||||||||||| |
Db    150 GGCTGGGGGCGCCTCAGCAG 131
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RESULT 6
BG284879/c
LOCUS       BG284879                683 bp    mRNA    linear   EST 21-FEB-2001
DEFINITION  602409113F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4538187 5',
            mRNA sequence.
ACCESSION   BG284879
VERSION     BG284879.1  GI:13036277
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 683)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10464  row: i  column: 04
            High quality sequence stop: 678.
FEATURES             Location/Qualifiers
     source          1. .683
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4538187"
                     /clone_lib="NIH_MGC_91"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.4 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      127 a    203 c    209 g    144 t
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 10;  Length 683;
  Best Local Similarity  95.0%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCGG 20
          |||||||||||||||||| |
Db    190 GGCTGGGGGCGCCTCAGCAG 171


RESULT 7
BI915042/c
LOCUS       BI915042                853 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603177231F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5241774 5',
            mRNA sequence.
ACCESSION   BI915042
VERSION     BI915042.1  GI:16179135
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11609  row: m  column: 07
            High quality sequence stop: 840.
FEATURES             Location/Qualifiers
     source          1. .853
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5241774"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      161 a    269 c    229 g    194 t
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 10;  Length 853;
  Best Local Similarity  95.0%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCGG 20
          |||||||||||||||||| |
Db    161 GGCTGGGGGCGCCTCAGCAG 142


RESULT 8
AL553611/c
LOCUS       AL553611                950 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL553611 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI078YB15 5
            prime, mRNA sequence.
ACCESSION   AL553611
VERSION     AL553611.1  GI:12893606
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 950)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .950
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DI078YB15"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      183 a    291 c    262 g    210 t      4 others
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 9;  Length 950;
  Best Local Similarity  95.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCGG 20
          |||||||||||||||||| |
Db    148 GGCTGGGGGCGCCTCAGCAG 129
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```
RESULT 9
BI519989/c
LOCUS       BI519989                995 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603071783F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163669 5',
            mRNA sequence.
ACCESSION   BI519989
VERSION     BI519989.1  GI:15344781
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 995)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11406  row: f  column: 22
            High quality sequence start: 30
            High quality sequence stop: 687.
FEATURES             Location/Qualifiers
     source          1. .995
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5163669"
                     /clone_lib="NIH_MGC_119"
                     /tissue_type="medulla"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source normal medulla from
                     anonymous male age 27.  Library  is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.3 kb, insert size range
                     0.9-3 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 013. Note:
                     this is a NIH_MGC Library."
BASE COUNT      185 a    283 c    314 g    213 t
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 10;  Length 995;
  Best Local Similarity  95.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           |||||||||||||||||| |
Db     575 GGCTGGGGGCGCCTCAGCAG 556


RESULT 10
BE337782/c
LOCUS       BE337782                568 bp    mRNA    linear   EST 14-JUL-2000
DEFINITION  894048D05.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
            Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION   BE337782
VERSION     BE337782.1  GI:9210867
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii.
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 568)
  AUTHORS   Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
            McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
  TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants; project phase 2
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Elizabeth H. Harris
            DCMB Box 91000
            Duke University
            Durham, NC 27708-1000, USA
            Tel: 919 613 8164
            Fax: 919 613 8177
            Email: chlamy@duke.edu.
FEATURES             Location/Qualifiers
     source          1. .568
                     /organism="Chlamydomonas reinhardtii"
                     /strain="CC-1690 wild type mt+ 21gr"
                     /db_xref="taxon:3055"
                     /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                     II"
                     /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                     XhoI; This library, constructed by John Davies and Jeffrey
                     McDermott, combines cDNAs from CC-1690 cells grown to
                     mid-log phase in TAP (acetate-containing) medium in the
                     light, TAP medium in the dark, HS (minimal) medium in
                     ambient levels of CO2 and HS medium bubbled with 5% CO2.
                     PolyA mRNA was purified from each sample, pooled and cDNA
                     synthesized. The cDNA was directionally cloned into lambda
                     ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
                     pBluescript II SK- plasmids were excised from the lambda
                     ZAP clones by superinfection with ExAssist (Stratagene)
                     phage. The library was normalized using method 4 described
                     in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT      123 a    177 c    143 g    125 t
ORIGIN

  Query Match            87.0%;  Score 17.4;  DB 10;  Length 568;
  Best Local Similarity  94.7%;  Pred. No. 3.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 GCTGGGGGCGCCTCAGCGG 20
           ||||||||||||||||||  |
Db     348 GCTGGGGGCGCCTCAGCCG 330


RESULT 11
BI722560/c
LOCUS       BI722560                610 bp    mRNA    linear   EST 19-SEP-2001
DEFINITION  1031062G07.y1 C. reinhardtii CC-1690, Stress II (normalized),
            Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION   BI722560
VERSION     BI722560.1  GI:15698255
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii.
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre
            ,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
  TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants. Project: 1031
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Charles Hauser
            DCMB Box 91000
            Duke University
            Durham, NC 27708-1000
            Tel: 919 613 8159
            Fax: 919 613 8177
            Email: chauser@duke.edu.
FEATURES             Location/Qualifiers
     source          1. .610
                     /organism="Chlamydomonas reinhardtii"
                     /strain="CC-1690 wild type mt+ 21gr"
                     /db_xref="taxon:3055"
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/clone_lib="C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al.,(2000) Plant Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

BASE COUNT 134 a 188 c 158 g 130 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 610;
Best Local Similarity 94.7%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCTGGGGGCGCCTCAGCGG 20
||||||||||||||||| |
Db 345 GCTGGGGGCGCCTCAGCCG 327

RESULT 12
BI527454/c
LOCUS BI527454 642 bp mRNA linear EST 29-AUG-2001
DEFINITION 1024081G05.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BI527454
VERSION BI527454.1 GI:15368028
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 642)
AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre ,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1024b
JOURNAL Unpublished (2001)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES Location/Qualifiers
source 1. .642
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al. (1996) Genome Research 6: 791-806."
BASE COUNT 134 a 200 c 171 g 136 t 1 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 642;
Best Local Similarity 94.7%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCTGGGGGCGCCTCAGCGG 20
||||||||||||||||| |
Db 314 GCTGGGGGCGCCTCAGCCG 296

RESULT 13
BI719349/c
LOCUS BI719349 668 bp mRNA linear EST 19-SEP-2001
DEFINITION 1031042H11.y1 C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BI719349
VERSION BI719349.1 GI:15695028
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 668)
AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre ,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
JOURNAL Unpublished (2001)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES Location/Qualifiers
source 1. .668
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al.,(2000) Plant Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
BASE COUNT 145 a 206 c 178 g 139 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 668;
Best Local Similarity 94.7%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCTGGGGGCGCCTCAGCGG 20
||||||||||||||||| |

```
Db    355 GCTGGGGGCGCCTCAGCCG 337


RESULT 14
BG845027/c
LOCUS       BG845027                675 bp    mRNA    linear   EST 29-MAY-2001
DEFINITION  1024008E07.y2 C. reinhardtii CC-1690, normalized, Lambda Zap II
            Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION   BG845027
VERSION     BG845027.1  GI:14226211
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii.
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 675)
  AUTHORS   Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
            McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
  TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants; project phase 2
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Charles Hauser
            DCMB Box 91000
            Duke University
            Durham, NC 27708-1000
            Tel: 919 613 8159
            Fax: 919 613 8177
            Email: chauser@duke.edu.
FEATURES             Location/Qualifiers
     source          1. .675
                     /organism="Chlamydomonas reinhardtii"
                     /strain="CC-1690 wild type mt+ 21gr"
                     /db_xref="taxon:3055"
                     /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                     II"
                     /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                     XhoI; This library, constructed by John Davies and Jeffrey
                     McDermott, combines cDNAs from CC-1690 cells grown to
                     mid-log phase in TAP (acetate-containing) medium in the
                     light, TAP medium in the dark, HS (minimal) medium in
                     ambient levels of CO2 and HS medium bubbled with 5% CO2.
                     PolyA mRNA was purified from each sample, pooled and cDNA
                     synthesized. The cDNA was directionally cloned into lambda
                     ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
                     pBluescript II SK- plasmids were excised from the lambda
                     ZAP clones by superinfection with ExAssist (Stratagene)
                     phage. The library was normalized using method 4 described
                     in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT      145 a    209 c    178 g    142 t      1 others
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 10;  Length 675;
  Best Local Similarity   94.7%;  Pred. No. 3.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 GCTGGGGGCGCCTCAGCGG 20
           |||||||||||||||||| |
Db     340 GCTGGGGGCGCCTCAGCCG 322


RESULT 15
BG845026/c
LOCUS       BG845026                684 bp    mRNA    linear   EST 29-MAY-2001
DEFINITION  1024008E07.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
            Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION   BG845026
VERSION     BG845026.1  GI:14226210
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii.
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
            McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
  TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants; project phase 2
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Charles Hauser
            DCMB Box 91000
            Duke University
            Durham, NC 27708-1000
            Tel: 919 613 8159
            Fax: 919 613 8177
            Email: chauser@duke.edu.
FEATURES             Location/Qualifiers
     source          1. .684
                     /organism="Chlamydomonas reinhardtii"
                     /strain="CC-1690 wild type mt+ 21gr"
                     /db_xref="taxon:3055"
                     /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                     II"
                     /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                     XhoI; This library, constructed by John Davies and Jeffrey
                     McDermott, combines cDNAs from CC-1690 cells grown to
                     mid-log phase in TAP (acetate-containing) medium in the
                     light, TAP medium in the dark, HS (minimal) medium in
                     ambient levels of CO2 and HS medium bubbled with 5% CO2.
                     PolyA mRNA was purified from each sample, pooled and cDNA
                     synthesized. The cDNA was directionally cloned into lambda
                     ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
                     pBluescript II SK- plasmids were excised from the lambda
                     ZAP clones by superinfection with ExAssist (Stratagene)
                     phage. The library was normalized using method 4 described
                     in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT      149 a    211 c    177 g    144 t      3 others
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 10;  Length 684;
  Best Local Similarity   94.7%;  Pred. No. 3.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 GCTGGGGGCGCCTCAGCGG 20
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Db     339 GCTGGGGGCGCCTCAGCCG 321


Search completed: November  2, 2002, 17:57:22
Job time : 723.455 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 13:09:44 ; Search time 82.7273 Seconds
(without alignments)
415.078 Million cell updates/sec

Title: US-09-856-803-10
Perfect score: 20
Sequence: 1 ggctgggggcgcctcagcag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	21	AAA46130	Human beta2 adrene
c	2	20	100.0	2300	20	AAX61116	Human beta2-adrene
c	3	20	100.0	2305	21	AAA38340	Human beta-adrener
c	4	20	100.0	3451	20	AAZ00774	Human beta 2-adren
c	5	20	100.0	3451	20	AAZ00775	Human beta 2-adren
c	6	20	100.0	3451	20	AAZ00777	Human beta 2-adren
c	7	20	100.0	3451	20	AAZ00778	Human beta 2-adren
c	8	20	100.0	3451	20	AAZ00780	Human beta 2-adren
	9	18.4	92.0	20	21	AAA46129	Human beta2 adrene
c	10	18.4	92.0	51	22	AAH79739	Human DNA containi
c	11	18.4	92.0	230	22	AAH27139	Human beta-2 adren
c	12	18.4	92.0	1999	18	AAT93250	Beta-2 adrenalin r
c	13	18.4	92.0	2340	21	AAA38784	Human beta2 adrene
c	14	18.4	92.0	3451	19	AAV52614	Human beta-2-adren
c	15	18.4	92.0	3451	20	AAZ00776	Human beta 2-adren
c	16	18.4	92.0	3451	20	AAZ00779	Human beta 2-adren
c	17	18.4	92.0	3451	20	AAZ00773	Human beta 2-adren
c	18	18.4	92.0	3451	21	AAA38339	Human beta-adrener
c	19	18.4	92.0	3451	24	AAS18444	Reference sequence
	20	17.4	87.0	472	22	ABA43331	Human breast cell
	21	17.4	87.0	472	22	ABA53772	Human foetal liver
	22	17.4	87.0	472	22	ABA23521	Probe #1987 for ge
	23	17.4	87.0	472	22	AAK02034	Human brain expres
	24	17.4	87.0	472	22	AAK27490	Human bone marrow
	25	17.4	87.0	472	22	AAI12067	Probe #2000 for ge
	26	17.4	87.0	472	22	AAI33402	Probe #2088 used t
	27	17.4	87.0	472	22	AAI01990	Probe #1981 used t
	28	16.8	84.0	50	22	AAL31184	Human SNP oligonuc
c	29	16.8	84.0	688	22	AAH05886	Human cDNA clone (
c	30	16.8	84.0	1926	20	AAZ21254	Human growth-relat
c	31	16.8	84.0	1926	20	AAV79600	Human growth-relat
c	32	16.8	84.0	2687	22	AAH16062	Human cDNA sequenc
c	33	16.8	84.0	3986	21	AAC75861	Human ORFX ORF1416
	34	16.8	84.0	4151	21	AAC59056	Human secreted pro
	35	16.4	82.0	1559	22	AAI99074	Human excretory re
	36	16.4	82.0	1559	22	AAI63424	Human kidney relat
c	37	16.4	82.0	2491	22	AAI60311	Human polynucleoti
	38	16.4	82.0	2499	22	AAI99075	Human excretory re
	39	16.4	82.0	2499	22	AAI63425	Human kidney relat
	40	16.4	82.0	2527	22	AAI58525	Human polynucleoti
c	41	15.8	79.0	65	23	AAS48769	Pseudomonas aerugi
c	42	15.8	79.0	175	16	AAT26811	Human gene signatu
	43	15.8	79.0	275	21	AAC01503	Human secreted pro
c	44	15.8	79.0	379	21	AAF15611	Human prostate can
c	45	15.8	79.0	400	21	AAC81042	Human secreted pro

ALIGNMENTS

RESULT 1
AAA46130
ID AAA46130 standard; DNA; 20 BP.
XX
AC AAA46130;
XX
DT 05-OCT-2000 (first entry)
XX
DE Human beta2 adrenergic receptor beta2AR T allele-specific primer #2.
XX
KW Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW congestive heart failure; ischemic heart disease; arrhythmia;
KW obesity; diabetes; vascular disease; premature labour; migraine;
KW anaphylaxis; chronic obstructive pulmonary disease;
KW allele-specific oligonucleotide primer; ss.
XX
OS Homo sapiens.
XX
PN WO200031307-A1.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US27963.
XX
PR 25-NOV-1998; 98US-0109886.
XX
PA (UYCI-) UNIV CINCINNATI.
XX
PI Liggett SB;
XX
DR WPI; 2000 400107/34.

XX
PT Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT receptor (beta 2 AR), useful for predicting genetic disposition to a
PT disease modified by beta 2 AR expression e.g. congestive heart failure,
PT hypertension -
XX
PS Claim 8; Page 12; 56pp; English.
XX
CC The present sequence is an allele-specific oligonucleotide primer
CC for the T allele of the human beta2 adrenergic receptor (beta2AR) gene,
CC which is located on chromosome 5q31 (12). The gene has two different
CC alleles, and it has been shown that the presence of two copies of the T
CC allele leads to higher expression of the gene. This is because the
CC polymorphism is found in the 5' leader sequence, which encodes a peptide
CC which regulates expression of the beta2AR gene. The polymorphism is
CC thought to affect individuals' responses to beta-agonists and
CC beta-antagonists, and is likely to influence their predisposition to
CC asthma, hypertension, congestive heart failure, ischemic heart disease,
CC arrhythmia, obesity, diabetes, vascular disease, premature labour,
CC migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD).
CC The gene can, therefore, be used to predict the susceptibility of an
CC individual to these diseases and determine the best treatment.
XX
SQ Sequence 20 BP; 2 A; 6 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGGGCGCCTCAGCAG 20
||||||||||||||||||||
Db 1 GGCTGGGGGCGCCTCAGCAG 20

RESULT 2
AAX61116/c
ID AAX61116 standard; DNA; 2300 BP.
XX
AC AAX61116;
XX
DT 27-JUL-1999 (first entry)
XX
DE Human beta2-adrenergic receptor gene.
XX
KW Alpha1B-adrenergic receptor; human; cardiovascular disease;
KW beta2 adrenergic receptor; genetic variation identification; hypertrophy;
KW disease diagnosis; hypertension; prostatic disease; pulmonary disorder;
KW asthma; peripheral vascular disorder; neuropsychic disorder;
KW endocrine-metabolic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO9924454-A1.
XX
PD 20-MAY-1999.
XX
PF 04-NOV-1998; 98WO-US23496.
XX
PR 10-NOV-1997; 97US-0086232.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Buescher R, Herrmann V, Insel PA;
XX
DR WPI; 1999-327357/27.
XX
PT Pairs of oligonucleotides for amplifying adrenergic receptor genes
XX
PS Disclosure; Fig 2; 58pp; English.
XX
CC This sequence represents the human beta2-adrenergic receptor gene, and
CC is amplified by the primers of the invention. The primers are non-self
CC hybridising; contain at least 15 nucleotides (nt) and has a melting
CC temperature 50-85 deg. C. Each pair of primers is: non-cross-hybridising;
CC anneals to two distinct segments (separated by at least 400 nt); and
CC generates a homogeneous population of gene segments in a polymerase chain
CC reaction (PCR). At least one primer in the pair can extend a 3'-end
CC sequence complementary to a template sequence in a DNA polymerase
CC reaction. The primers are used to amplify segments of the alpha1B and
CC beta2 adrenergic receptor genes, particularly to identify genetic
CC variations for diagnosis of disease. Specifically variations in the
CC alpha1B gene are associated with cardiovascular disease, hypertension and
CC prostatic disease (hypertrophy), and those in the beta2 gene with
CC cardiovascular disease, hypertension and asthma, but variations may also
CC be associated with peripheral vascular, pulmonary, neuropsychic and
CC endocrine-metabolic disorders. These primers allow rapid and specific
CC amplification of large and homogeneous gene segments of the alpha1B and
CC beta2 genes from a complex mixture of DNAs. This makes possible detection
CC of genetic alterations not previously amenable to routine, automated and
CC large-scale sequencing analysis.
XX
SQ Sequence 2300 BP; 495 A; 613 C; 646 G; 546 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 2300;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGGGCGCCTCAGCAG 20
||||||||||||||||||||
Db 765 GGCTGGGGGCGCCTCAGCAG 746

RESULT 3
AAA38340/c
ID AAA38340 standard; DNA; 2305 BP.
XX
AC AAA38340;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human beta-adrenergic receptor-2 coding region.
XX
KW Beta-adrenergic receptor-2 gene; coding region;
KW polymorphism; polymorphic marker; cardiovascular disease;
KW myocardial infarction; unstable angina; hypertension; atherosclerosis;
KW stroke; prognosis; drug screening; treatment outcome; human; ds.
XX
OS Homo sapiens.
XX
PN WO200022166-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-IB01678.
XX
PR 14-OCT-1998; 98US-0104286.
PR 14-OCT-1998; 98US-0104302.
XX
PA (EURO-) EURONA MEDICAL AB.
XX
PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
XX
DR WPI; 2000-318010/27.
XX
PT Assessing cardiovascular status in humans involves comparing test
PT polymorphic pattern comprising polymorphic positions within genes
PT encoding specific proteins, with reference polymorphic pattern -
XX
PS Disclosure; Page 124-125; 126pp; English.
XX
CC The invention relates to a novel method of assessing the cardiovascular
CC status in an individual and to newly identified polymorphisms in the
CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II
CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
CC aldosterone synthase, endothelin receptor type A and beta-adrenergic
CC receptors 1 and 2. The method comprises determining the sequence at one

```
CC   or more polymorphic positions within these genes, and comparing the
CC   pattern of polymorphisms from the individual with a reference polymorphic
CC   pattern obtained from a population of individuals exhibiting a
CC   predetermined cardiovascular disease status. The polymorphic markers are
CC   useful for determining the predisposition of an individual to
CC   cardiovascular disorders such as myocardial infarction, unstable angina,
CC   hypertension, atherosclerosis and stroke. They are also useful for
CC   predicting the likely cardiovascular status of a patient given a
CC   treatment regimen comprising administration of cardiovascular drugs
CC   (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
CC   blockers) or calcium channel blockers). One or more polymorphic markers
CC   provides a basis for predicting the outcome of a treatment regimen.
CC   Fragments of the genes comprising a polymorphic site may be used as
CC   primers and probes for detecting genetic polymorphisms or in molecular
CC   library arrays for high throughput screening. The genes, and the proteins
CC   they encode are useful in the screening of potential cardiovascular
CC   drugs. Determination of an individual's polymorphic pattern reduces or
CC   eliminates trial and error in selecting a treatment for a particular
CC   individual cardiovascular patient. It also provides the ability to
CC   eliminate patients from clinical trials who are predicted to be
CC   non-responsive, or at a risk for an adverse response, to a particular
CC   treatment regimen. Adverse results in an early trial can be evaluated to
CC   identify polymorphic patterns so that the adverse results can be
CC   correlated with a sub-population of the test population, permitting
CC   exclusion of such sub-populations from the treatment group. Beneficial
CC   drugs can be approved for use in the appropriate population, thereby
CC   decreasing the number of patients required for a clinical trial, which in
CC   turn decreases the duration and cost of such trials. The present
CC   sequence represents the human beta-adrenergic receptor-2 gene
CC   coding region (GenBank Y00106/g293708). The polymorphic sites identified
CC   are 839A/G, 872C/G, 1045A/G, 1284C/T, 1316A/C, 1846C/G, 2032A/G,
CC   2068 no insert/G/C and 2070 no insert/C.
XX
SQ   Sequence 2305 BP; 495 A; 616 C; 649 G; 545 T; 0 other;

  Query Match            100.0%;  Score 20;  DB 21;  Length 2305;
  Best Local Similarity  100.0%;  Pred. No. 8.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db     765 GGCTGGGGGCGCCTCAGCAG 746


RESULT 4
AAZ00774/c
ID   AAZ00774 standard; DNA; 3451 BP.
XX
AC   AAZ00774;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 1.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(159,t)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(245,a)
FT                   /*tag=  b
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(565,g)
FT                   /*tag=  c
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(934,g)
FT                   /*tag=  d
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1120,g)
FT                   /*tag=  e
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1221,c)
FT                   /*tag=  f
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1541,t)
FT                   /*tag=  g
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
FT   mutation        replace(1568,t)
FT                   /*tag=  h
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1633,a)
FT                   /*tag=  i
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
FT   mutation        replace(1666,c)
FT                   /*tag=  j
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Glu
FT                          residue to Gln residue"
FT   mutation        replace(1839,g)
FT                   /*tag=  k
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(2078,c)
FT                   /*tag=  l
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Ile
FT                          residue to Thr residue"
FT   mutation        replace(2110,c)
FT                   /*tag=  m
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(2640,g)
FT                   /*tag=  n
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(2826,g)
FT                   /*tag=  o
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
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```
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 2; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 794 A; 871 C; 892 G; 894 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCAG 1540


RESULT 5
AAZ00775/c
ID   AAZ00775 standard; DNA; 3451 BP.
XX
AC   AAZ00775;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 2.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1541,c)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 3; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 790 A; 872 C; 895 G; 894 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCAG 1540


RESULT 6
AAZ00777/c
ID   AAZ00777 standard; DNA; 3451 BP.
XX
AC   AAZ00777;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 4.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
```

```
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1541,c)
FT                   /*tag= a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
FT   mutation        replace(1633,a)
FT                   /*tag= b
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 5; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 789 A; 872 C; 896 G; 894 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCAG 1540


RESULT 7
AAZ00778/c
ID   AAZ00778 standard; DNA; 3451 BP.
XX
AC   AAZ00778;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 5.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1541,c)
FT                   /*tag= a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 6; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 790 A; 872 C; 895 G; 894 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          ||||||||||||||||||||
Db   1559 GGCTGGGGGCGCCTCAGCAG 1540


RESULT 8
AAZ00780/c
ID   AAZ00780 standard; DNA; 3451 BP.
XX
AC   AAZ00780;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 7.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1541,t)
FT                   /*tag=  g
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
FT   mutation        replace(1633,a)
FT                   /*tag=  b
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997    97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 8; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 789 A; 872 C; 896 G; 894 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          ||||||||||||||||||||
Db   1559 GGCTGGGGGCGCCTCAGCAG 1540


RESULT 9
AAA46129
ID   AAA46129 standard; DNA; 20 BP.
XX
AC   AAA46129;
XX
DT   05-OCT-2000  (first entry)
XX
DE   Human beta2 adrenergic receptor beta2AR C allele-specific primer #2.
XX
KW   Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW   chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW   congestive heart failure; ischemic heart disease; arrhythmia;
KW   obesity; diabetes; vascular disease; premature labour; migraine;
KW   anaphylaxis; chronic obstructive pulmonary disease;
KW   allele-specific oligonucleotide primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200031307-A1.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US27963.
XX
PR   25-NOV-1998;   98US-0109886.
XX
PA   (UYCI-) UNIV CINCINNATI.
XX
PI   Liggett SB;
XX
DR   WPI; 2000-400107/34.
XX
PT   Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT   receptor (beta 2 AR), useful for predicting genetic disposition to a
PT   disease modified by beta 2 AR expression e.g. congestive heart failure,
PT   hypertension -
XX
PS   Claim 8; Page 12; 56pp; English.
XX
CC   The present sequence is an allele-specific oligonucleotide primer
CC   for the C allele of the human beta2 adrenergic receptor (beta2AR) gene,
CC   which is located on chromosome 5q31 (12). The gene has two different
CC   alleles, and it has been shown that the presence of two copies of the T
CC   allele leads to higher expression of the gene. This is because the
CC   polymorphism is found in the 5' leader sequence, which encodes a peptide
CC   which regulates expression of the beta2AR gene. The polymorphism is
CC   thought to affect individuals' responses to beta-agonists and
CC   beta-antagonists, and is likely to influence their predisposition to
CC   asthma, hypertension, congestive heart failure, ischemic heart disease,
CC   arrhythmia, obesity, diabetes, vascular disease, premature labour,
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CC   migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD).
CC   The gene can, therefore, be used to predict the susceptibility of an
CC   individual to these diseases and determine the best treatment.
XX
SQ   Sequence 20 BP; 1 A; 6 C; 11 G; 2 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 21;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 43;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           |||||||||||||||||| |
Db       1 GGCTGGGGGCGCCTCAGCGG 20


RESULT 10
AAH79739/c
ID   AAH79739 standard; DNA; 51 BP.
XX
AC   AAH79739;
XX
DT   19-SEP-2001  (first entry)
XX
DE   Human DNA containing single nucleotide polymorphism SEQ ID NO. 354.
XX
KW   Human; single nucleotide polymorphism; SNP; angiopoietin;
KW   4-hydroxybutyrate; dehydrogenase; protein therapy;
KW   adenosine triphosphate-dependent RNA helicase;
KW   major histocompatibility complex Class I histocompatibility antigen; MHC;
KW   phosphoglycerate kinase; immunosuppressive; immunostimulatory;
KW   antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
KW   antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; ds.
XX
OS   Homo sapiens.
XX
PN   WO200148245-A2.
XX
PD   05-JUL-2001.
XX
PF   27-DEC-2000; 2000WO-US35346.
XX
PR   27-DEC-1999;   99US-0472688.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-418297/44.
XX
PT   Polymorphic nucleic acids encoding e.g. angiopoietin, dehydrogenase,
PT   adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
PT   kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
PT   diseases and infections -
XX
PS   Claim 1; Page 162; 484pp; English.
XX
CC   The invention relates to nucleic acids (AAH79386-AAH80036) encoding
CC   polymorphic variants of proteins (AAG98010-AAG98238) related to
CC   angiopoietin, 4-hydroxybutyrate, dehydrogenase, adenosine trip osphate
CC   (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
CC   Class I histocompatibility antigen and/or phosphoglycerate kinase. These
CC   nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
CC   proteins have potential immunosuppressive, immunostimulatory,
CC   antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
CC   antileukemic, neuroprotective and antimicrobial activity and may be
CC   useful in gene/protein therapy, vaccines, modulation of the expression
CC   and activity of proteins related to angiopoietin, 4-hydroxybutyrate,
CC   dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase,
CC   major histocompatibility complex (MHC) Class I histocompatibility antigen
CC   and/or phosphoglycerate kinase. Disorders that may be prevented,
CC   diagnosed and/or treated by the above methods include multifactorial
CC   diseases with a genetic component, such as autoimmune diseases (e.g.
CC   rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
CC   erythematosus and Grave's disease), inflammation, cancer (e.g. cancers
CC   of the bladder, brain, breast, colon and kidney, leukemia), diseases of
CC   the nervous system, an infection of pathogenic organisms. They may also
CC   be used to alter phenotypic traits such as longevity, appearance,
CC   strength, speed and endurance.
XX
SQ   Sequence 51 BP; 5 A; 24 C; 18 G; 4 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 22;  Length 51;
  Best Local Similarity   95.0%;  Pred. No. 43;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           |||||||||||||||||| |
Db      44 GGCTGGGGGCGCCTCAGCGG 25


RESULT 11
AAH27139/c
ID   AAH27139 standard; DNA; 230 BP.
XX
AC   AAH27139;
XX
DT   08-AUG-2001  (first entry)
XX
DE   Human beta-2 adrenergic receptor UTR region with RBP binding ability.
XX
KW   Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration;
KW   stroke; cardiovascular disease; hypertension; cancer; inflammation;
KW   metabolic disorder; obesity; diabetes; beta-2 adrenergic receptor; ds.
XX
OS   Homo sapiens.
XX
PN   WO200134621-A1.
XX
PD   17-MAY-2001.
XX
PF   09-NOV-2000; 2000WO-US30888.
XX
PR   10-NOV-1999;   99US-0437458.
XX
PA   (MESS-) MESSAGE PHARM INC.
XX
PI   Giordano A,  Xavier AK;
XX
DR   WPI; 2001-335904/35.
XX
PT   New nucleic acids that bind RNA-binding proteins or regulate mRNA
PT   function, useful for therapeutic gene regulation, such as in cases of
PT   neurodegeneration  -
XX
PS   Claim 1; Page 28; 33pp; English.
XX
CC   Sequences AAH27132 - AAH27151 represent human gene untranslated regions
CC   where the corresponding mRNA fragment has RNA binding protein (RBP)
CC   binding activity. RBPs mediate the processing of pre-mRNA, the transport
CC   of mRNA from the nucleus to the cytoplasm, mRNA stabilisation,
CC   translational efficiency, and the sequestration of some mRNAs. Therefore
CC   modification of post-transcriptional protein expression in eukaryotic
CC   cells may be carried out through the targeting specific interactions of
CC   proteins that bind to RBPs. The gene fragments of the invention are used
CC   to identify their optimized sub-fragments, compounds that affect RNA/RBP
CC   interaction or mRNA functionality; or RBPs that interact with the
CC   compounds. Compounds identified using the gene fragments are potentially
CC   useful for therapeutic regulation of gene expression, such as in cases of
CC   neurodegeneration; stroke; cardiovascular disease; hypertension; cancer;
CC   inflammation; metabolic disorders (obesity and diabetes) and bacterial or
CC   viral infection. The present sequence is one of gene fragments of the
CC   invention, isolated from the human beta-2 adrenergic receptor gene.
XX
SQ   Sequence 230 BP; 42 A; 91 C; 70 G; 27 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 22;  Length 230;
```

```
  Best Local Similarity   95.0%;  Pred. No. 44;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           |||||||||||||||||| |
Db     191 GGCTGGGGGCGCCTCAGCGG 172


RESULT 12
AAT93250/c
ID   AAT93250 standard; cDNA to mRNA; 1999 BP.
XX
AC   AAT93250;
XX
DT   20-APR-1998  (first entry)
XX
DE   Beta-2 adrenalin receptor subtype coding sequence.
XX
KW   Beta-2 adrenalin subtype; cyanopindrol; agonist; antagonist;
KW   asthmatic disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             190..1431
FT                   /*tag=  a
XX
PN   WO9735963-A1.
XX
PD   02-OCT-1997.
XX
PF   24-MAR-1997;    97WO-JP00982.
XX
PR   27-MAR-1996;    96JP-0072914.
XX
PA   (DAIN ) DAINIPPON PHARM CO LTD.
XX
PI   Fujii K,  Furutani Y,  Kawashima H,  Nomura A,  Yano K;
XX
DR   WPI; 1997-489627/45.
DR   P-PSDB; AAW34320.
XX
PT   Novel beta-2 adrenalin receptor sub-type - useful for screening for
PT   agonists and antagonists and researching asthmatic diseases
XX
PS   Disclosure; Page 27-30; 47pp; Japanese.
XX
CC   This sequence encodes the protein of the invention. The protein of the
CC   invention is a beta-2 adrenalin receptor subtype with Kd value of
CC   approximately 75 pM against 125I-cyanopindrol. The protein can be used in
CC   screening for agonists and antagonists, which are useful in researching
CC   asthmatic diseases.
XX
SQ   Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 18;  Length 1999;
  Best Local Similarity   95.0%;  Pred. No. 44;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           |||||||||||||||||| |
Db     161 GGCTGGGGGCGCCTCAGCGG 142


RESULT 13
AAA38784/c
ID   AAA38784 standard; DNA; 2340 BP.
XX
AC   AAA38784;
XX
DT   05-OCT-2000  (first entry)
XX
DE   Human beta2 adrenergic receptor beta2AR gene.
XX
KW   Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW   chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW   congestive heart failure; ischemic heart disease; arrhythmia;
KW   obesity; diabetes; vascular disease; premature labour; migraine;
KW   anaphylaxis; chronic obstructive pulmonary disease; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1487..2340
FT                   /*tag=  a
FT                   /product= "beta2 adrenergic receptor"
FT                   /note= "no stop codon given at 3' end of sequence"
FT                   /partial
FT   sig_peptide     1487..1546
FT                   /*tag=  b
FT                   /label= 5'_leader_cistron
FT   allele          replace(1541,T)
FT                   /*tag=  c
FT   mat_peptide     1588..2340
FT                   /*tag=  d
XX
PN   WO200031307-A1.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;    99WO-US27963.
XX
PR   25-NOV-1998;    98US-0109886.
XX
PA   (UYCI-) UNIV CINCINNATI.
XX
PI   Liggett SB;
XX
DR   WPI; 2000-400107/34.
XX
PT   Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT   receptor , eta 2 AR), useful for predicting genetic disposition to a
PT   disease modified by beta 2 AR expression e.g. congestive heart failure,
PT   hypertension -
XX
PS   Disclosure; Figure 1; 56pp; English.
XX
CC   The present sequence is a fragment of the C allele of the human beta2
CC   adrenergic receptor (beta2AR) gene, which is located on chromosome
CC   5q31 (12). The gene has two different alleles, and it has been shown that
CC   the presence of two copies of the T allele leads to higher expressio: of
CC   the gene. This is because the polymorphism is found in the 5' leader
CC   sequence, which encodes a peptide which regulates expression of the
CC   beta2AR gene. The polymorphism is thought to affect individuals'
CC   responses to beta-agonists and beta-antagonists, and is likely to
CC   influence their predisposition to asthma, hypertension,
CC   congestive heart failure, ischemic heart disease, arrhythmia, obesity,
CC   diabetes, vascular disease, premature labour, migraine, anaphylaxis and
CC   chronic obstructive pulmonary disease (COPD). The gene can, therefore, be
CC   used to predict the susceptibility of an individual to these diseases and
CC   determine the best treatment.
XX
SQ   Sequence 2340 BP; 498 A; 627 C; 653 G; 562 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 21;  Length 2340;
  Best Local Similarity   95.0%;  Pred. No. 44;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           |||||||||||||||||| |
Db    1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 14
AAV52614/c
ID   AAV52614 standard; cDNA; 3451 BP.
```

```
XX
AC   AAV52614;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Human beta-2-adrenergic receptor cDNA.
XX
KW   Beta-2-adrenergic receptor; human; asthma; beta-agonist;
KW   polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1588..2829
FT                   /*tag=  a
FT   variation       1633
FT                   /*tag=  b
FT                   /note= "A to G substitution, results in Arg16
FT                          to Gly amino acid change"
XX
PN   WO9839477-A2.
XX
PD   11-SEP-1998.
XX
PF   26-FEB-1998;   98WO-US03908.
XX
PR   03-MAR-1997;   97US-0811441.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Boushey H,  Chinchilli VM,  Drazen JM,  Fish JE,  Ford JG;
PI   Martin RJ;
XX
DR   WPI; 1998-506372/43.
DR   P-PSDB; AAW75777.
XX
PT   Diagnosing asthma patients predisposed to adverse beta-agonist
PT   reactions upon regular administration - by identifying patients
PT   homozygous for allele encoding Arg at position 16 of
PT   beta2-adrenergic receptor protein
XX
PS   Disclosure; Page 33-35; 46pp; English.
XX
CC   This cDNA sequence codes for human beta-2-adrenergic receptor (see
CC   AAW75777) having an arginine residue at position 16.  A novel method
CC   for identifying individuals susceptible to adverse responses to
CC   regular administration of beta-agonists comprises: (a) identifying
CC   in a genomic nucleic acid sample from the individual first and
CC   second alleles of the beta 2-adrenergic receptor gene, and (b)
CC   classifying an individual as susceptible if first and second
CC   alleles both encode Arg at residue 16 of the beta 2-adrenergic
CC   receptor protein.  Beta 2-adrenergic receptor gene alleles may be
CC   identified by any known method e.g. denaturing gel electrophoresis
CC   or PCR amplification (see also AAV52615-17).  Identification
CC   preferably comprises amplifying a portion of each allele which
CC   includes the sequence encoding residue 16, and optionally also
CC   comprises determining nucleotide sequences of these portions (e.g.
CC   by automated sequence analysis).  The invention identifies a known
CC   polymorphism in the beta 2-adrenergic receptor gene as being linked
CC   to adverse responses to regular beta-agonist administration;
CC   position 16 of the encoded protein can be either Arg or Gly, and
CC   individuals homozygous for Arg16 are more susceptible.
XX
SQ   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 19;  Length 3451;
  Best Local Similarity   95.0%;  Pred. No. 44;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||| |
Db    1559 GGCTGGGGGCGCCTCAGCGG 1540
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RESULT 15
AAZ00776/c
ID   AAZ00776 standard; DNA; 3451 BP.
XX
AC   AAZ00776;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 3.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1633,a)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                           nucleic acid sequence represented in AAZ00773
FT                           and results in a change in the corresponding
FT                           wild type amino acid sequence from an Gly
FT                           residue to Arg residue"
FT   mutation        replace(1666,c)
FT                   /*tag=  b
FT                   /note= "This nucleotide differs from the wild type
FT                           nucleic acid sequence represented in AAZ00773
FT                           and results in a change in the corresponding
FT                           wild type amino acid sequence from an Glu
FT                           residue to Gln residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 4; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
```

CC to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC 2-receptor agonists can be developed. Treatments can be optimized for
CC individuals, including gene therapy and pharmaceutical intervention
CC therapy. This sequence represents a variant of the wild type human beta
CC 2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ Sequence 3451 BP; 789 A; 872 C; 897 G; 893 T; 0 other;

Query Match 92.0%; Score 18.4; DB 20; Length 3451;
Best Local Similarity 95.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           |||||||||||||||||| |
Db    1559 GGCTGGGGGCGCCTCAGCGG 1540
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Search completed: November 2, 2002, 16:13:19
Job time : 83.7273 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 14:22:04 ; Search time 18.5455 Seconds
(without alignments)
264.899 Million cell updates/sec

Title: US-09-856-803-10
Perfect score: 20
Sequence: 1 ggctgggggcgcctcagcag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	18.4	92.0	230	4	US-09-437-457-8	Sequence 8, Appli
c	2	16.8	84.0	1926	2	US-08-978-182-2	Sequence 2, Appli
c	3	16.8	84.0	1926	2	US-09-205-681-2	Sequence 2, Appli
c	4	15.8	79.0	1642	1	US-08-723-938-2	Sequence 2, Appli
c	5	15.8	79.0	1642	2	US-09-080-538-2	Sequence 2, Appli
c	6	15.8	79.0	8906	2	US-08-826-267-1	Sequence 1, Appli
	7	15.2	76.0	500	4	US-08-818-112-101	Sequence 101, App
	8	15.2	76.0	500	4	US-08-818-111-96	Sequence 96, Appl
	9	15.2	76.0	500	4	US-09-056-556-101	Sequence 101, App
	10	15.2	76.0	2169	1	US-08-379-496-1	Sequence 1, Appli
c	11	15.2	76.0	3032	3	US-08-990-140-1	Sequence 1, Appli
c	12	15.2	76.0	3032	4	US-09-546-238-1	Sequence 1, Appli
c	13	15.2	76.0	7286	5	PCT-US95-11684-1	Sequence 1, Appli
c	14	14.8	74.0	105	3	US-08-717-294-81	Sequence 81, Appl
	15	14.8	74.0	1600	2	US-08-487-113D-117	Sequence 117, App
	16	14.8	74.0	1600	2	US-08-720-420A-117	Sequence 117, App
	17	14.8	74.0	1992	4	US-09-276-531-19	Sequence 19, Appl
	18	14.8	74.0	2101	4	US-09-276-531-21	Sequence 21, Appl
c	19	14.8	74.0	2186	4	US-09-184-001-1	Sequence 1, Appli
	20	14.8	74.0	3271	2	US-08-852-806-1	Sequence 1, Appli
	21	14.8	74.0	3271	3	US-09-163-669-1	Sequence 1, Appli
c	22	14.8	74.0	4451	3	US-08-717-294-42	Sequence 42, Appl
	23	14.8	74.0	6816	4	US-09-404-650-1	Sequence 1, Appli
	24	14.8	74.0	6855	4	US-09-404-650-3	Sequence 3, Appli
	25	14.8	74.0	35060	3	US-08-814-095-7	Sequence 7, Appli
	26	14.8	74.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	27	14.8	74.0	4411529	4	US-09-103-840A-1	Sequence 1, Appli
c	28	14.2	71.0	248	4	US-09-020-956-77	Sequence 77, Appl
c	29	14.2	71.0	248	4	US-09-030-607-77	Sequence 77, Appl
c	30	14.2	71.0	248	4	US-09-439-313-77	Sequence 77, Appl
c	31	14.2	71.0	250	4	US-09-030-607-179	Sequence 179, App
c	32	14.2	71.0	250	4	US-09-439-313-179	Sequence 179, App
c	33	14.2	71.0	400	4	US-08-631-469B-3	Sequence 3, Appli
c	34	14.2	71.0	400	4	US-09-056-868B-3	Sequence 3, Appli
c	35	14.2	71.0	401	4	US-09-328-111-761	Sequence 761, App
c	36	14.2	71.0	403	3	US-08-476-705A-3	Sequence 3, Appli
c	37	14.2	71.0	570	1	US-08-469-667-13	Sequence 13, Appl
c	38	14.2	71.0	570	4	US-09-224-110-13	Sequence 13, Appl
c	39	14.2	71.0	570	5	PCT-US95-07289-13	Sequence 13, Appl
	40	14.2	71.0	807	1	US-08-270-584A-1	Sequence 1, Appli
	41	14.2	71.0	807	2	US-08-765-192-1	Sequence 1, Appli
	42	14.2	71.0	807	3	US-09-199-793-1	Sequence 1, Appli
c	43	14.2	71.0	821	4	US-08-352-902D-146	Sequence 146, App
	44	14.2	71.0	1026	4	US-07-751-891B-24	Sequence 24, Appl
	45	14.2	71.0	1028	4	US-08-118-200-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-09-437-457-8/c
; Sequence 8, Application US/09437457
; Patent No. 6273893
; GENERAL INFORMATION:
;  APPLICANT: Giordano, Anthony
;  APPLICANT: Xavier, Ashish
;  TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND METHODS FOR
;  TITLE OF INVENTION: IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
;  TITLE OF INVENTION: INTERACTIONS AND MRNA FUNCTIONALITY
;  FILE REFERENCE: 50093/014001
;  CURRENT APPLICATION NUMBER: US/09/437,457
;  CURRENT FILING DATE: 1999-11-10
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 230
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-437-457-8

  Query Match             92.0%;  Score 18.4;  DB 4;  Length 230;
  Best Local Similarity   95.0%;  Pred. No. 8.4;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
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Db     191 GGCTGGGGGCGCCTCAGCGG 172


RESULT 2
US-08-978-182-2/c
; Sequence 2, Application US/08978182
; Patent No. 5849556
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Yue, Henry
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Kaser, Matthew
;    APPLICANT:  Mathur, Preete
;    TITLE OF INVENTION:  HUMAN GROWTH-RELATED CDC10 HOMOLOG
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,182
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0426 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1926 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  TLYMNOT06
;      CLONE:  3003826
US-08-978-182-2

  Query Match             84.0%;  Score 16.8;  DB 2;  Length 1926;
  Best Local Similarity   90.0%;  Pred. No. 38;
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Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||| | ||||||||||||||||
Db     261 GGCGGTGGGCGCCTCAGCAG 242


RESULT 3
US-09-205-681-2/c
; Sequence 2, Application US/09205681
; Patent No. 5952214
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Yue, Henry
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Kaser, Matthew
;    APPLICANT:  Mathur, Preete
;    TITLE OF INVENTION:  HUMAN GROWTH-RELATED CDC10 HOMOLOG
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/205,681
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/978,182
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0426 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1926 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  TLYMNOT06
;      CLONE:  3003826
US-09-205-681-2

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  Best Local Similarity   90.0%;  Pred. No. 38;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||| | ||||||||||||||||
Db     261 GGCGGTGGGCGCCTCAGCAG 242


RESULT 4
US-08-723-938-2/c
; Sequence 2, Application US/08723938
; Patent No. 5776759
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Coleman, Roger
;    TITLE OF INVENTION:  TWO NOVEL HUMAN CATHESPIN PROTEINS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/723,938
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0125 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1642 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;    IMMEDIATE SOURCE:
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;      LIBRARY:  Consensus
;      CLONE:  Consensus
US-08-723-938-2

  Query Match             79.0%;  Score 15.8;  DB 1;  Length 1642;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GCTGGGGGCGCCTCAGCAG 20
           ||||||||| ||||| |||
Db    1228 GCTGGGGGCCCCTCATCAG 1210


RESULT 5
US-09-080-538-2/c
; Sequence 2, Application US/09080538
; Patent No. 5965129
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Coleman, Roger
;    TITLE OF INVENTION:  TWO NOVEL HUMAN CATHESPIN PROTEINS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/080,538
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/723,938
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0125 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1642 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;    IMMEDIATE SOURCE:
;      LIBRARY:  Consensus
;      CLONE:  Consensus
US-09-080-538-2

  Query Match             79.0%;  Score 15.8;  DB 2;  Length 1642;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GCTGGGGGCGCCTCAGCAG 20
           ||||||||| ||||| |||
Db    1228 GCTGGGGGCCCCTCATCAG 1210


RESULT 6
US-08-826-267-1/c
; Sequence 1, Application US/08826267
; Patent No. 5994070
;  GENERAL INFORMATION:
;    APPLICANT:  Streuli, Michel
;    TITLE OF INVENTION:  No. 5994070el TRIO Molecules and Uses Related Thereto
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/826,267
;      FILING DATE:  1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/014,214
;      FILING DATE:  27 MARCH (1996)
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Amy E. Mandragouras
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  DFN-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8906 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  67..8647
US-08-826-267-1

  Query Match             79.0%;  Score 15.8;  DB 2;  Length 8906;
  Best Local Similarity   89.5%;  Pred. No. 99;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GCTGGGGGCGCCTCAGCAG 20
           |||||||||||| | ||||
Db    6884 GCTGGGGGCGCCGCCGCAG 6866


RESULT 7
US-08-818-112-101
; Sequence 101, Application US/08818112
; Patent No. 6290969
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    APPLICANT:  Campos-Neto, Antonio
;    APPLICANT:  Houghton, Raymond
;    APPLICANT:  Vedvick, Thomas S.
;    APPLICANT:  Twardzik, Daniel R.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
;    TITLE OF INVENTION:  AND DIAGNOSIS OF TUBERCULOSIS
;    NUMBER OF SEQUENCES:  153
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
```

```
;       STREET:  6300 Columbia Center, 701 Fifth Avenue
;       CITY:  Seattle
;       STATE:  Washington
;       COUNTRY:  USA
;       ZIP:  98104-7092
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/818,112
;       FILING DATE:  13-MAR-1997
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Maki, David J.
;       REGISTRATION NUMBER:  31,392
;       REFERENCE/DOCKET NUMBER:  210121.411C6
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 622-4900
;       TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  101:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  500 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-818-112-101

  Query Match           76.0%;  Score 15.2;  DB 4;  Length 500;
  Best Local Similarity  85.0%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
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Db      25 GGCCGGGGTCGCCTCCGCAG 44


RESULT 8
US-08-818-111-96
; Sequence 96, Application US/08818111
; Patent No. 6338852
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    APPLICANT:  Campos-Neto, Antonia
;    APPLICANT:  Houghton, Raymond
;    APPLICANT:  Vedvick, Thomas S.
;    APPLICANT:  Twardzik, Daniel R.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR DIAGNOSIS OF    TUBERCULOSIS
;    NUMBER OF SEQUENCES:  148
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/818,111
;      FILING DATE:  13-MAR-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.417C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  96:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  500 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-818-111-96

  Query Match           76.0%;  Score 15.2;  DB 4;  Length 500;
  Best Local Similarity  85.0%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||| |||| |||||| ||||
Db      25 GGCCGGGGTCGCCTCCGCAG 44


RESULT 9
US-09-056-556-101
; Sequence 101, Application US/09056556
; Patent No. 6350456
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE PREVENTION AND            TRE
;    NUMBER OF SEQUENCES:  241
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/056,556
;      FILING DATE:  07-APR-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.457
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  101:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  500 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-056-556-101

  Query Match           76.0%;  Score 15.2;  DB 4;  Length 500;
  Best Local Similarity  85.0%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||| |||| |||||| ||||
Db      25 GGCCGGGGTCGCCTCCGCAG 44


RESULT 10
US-08-379-496-1
; Sequence 1, Application US/08379496
; Patent No. 5593833
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;  GENERAL INFORMATION:
;    APPLICANT:  MORRISON, Nigel A
;    APPLICANT:  EISMAN, John A
;    APPLICANT:  KELLY, Paul J
;    TITLE OF INVENTION:  Assessment of Trans-Acting Factors Allelic
;    TITLE OF INVENTION:  Variation
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rothwell, Figg, Ernst & Kurz
;      STREET:  Suite 701-E, 555 13th Street.N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/379,496
;      FILING DATE:  02-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, Barbara G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1871-114
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 783-6040
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2169 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-379-496-1

  Query Match             76.0%;  Score 15.2;  DB 1;  Length 2169;
  Best Local Similarity   85.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           |||||| |||  ||||||||
Db    2011 GGCTGGCGGCTACTCAGCAG 2030


RESULT 11
US-08-990-140-1/c
; Sequence 1, Application US/08990140A
; Patent No. 6093795
; GENERAL INFORMATION:
;  APPLICANT: Olsen, Henrik S.
;  APPLICANT: Ruben, Steven M.
;  APPLICANT: Sonenberg, Nahum
;  APPLICANT: Methot, Nathalie
;  APPLICANT: Rom, Eran
;  TITLE OF INVENTION: Human Prt1-like Subunit Protein (hPrt1) and Human
;  TITLE OF INVENTION: eIF4GF-like Protein (p97) Genes
;  FILE REFERENCE: 1488.0700001
;  CURRENT APPLICATION NUMBER: US/08/990,140A
;  CURRENT FILING DATE: 1997-12-12
;  EARLIER APPLICATION NUMBER: US 60/033,151
;  EARLIER FILING DATE: 1996-12-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3032
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (97)..(2718)
US-08-990-140-1

  Query Match             76.0%;  Score 15.2;  DB 3;  Length 3032;
  Best Local Similarity   85.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
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Db    2219 GGCCGGGGCCGCCACAGCAG 2200


RESULT 12
US-09-546-238-1/c
; Sequence 1, Application US/09546238
; Patent No. 6316225
; GENERAL INFORMATION:
;  APPLICANT:  Olsen, Henrik S.
;  APPLICANT:  Ruben, Steven M.
;  APPLICANT:  Sonenberg, Nahum
;  APPLICANT:  Methot, Nathalie
;  APPLICANT:  Rom, Eran
;  TITLE OF INVENTION:  Human Prt1-like Subunit Protein (hPrt1) Polynucleotides
;  TITLE OF INVENTION:  (as amended)
;  FILE REFERENCE:  1488.0700002
;  CURRENT APPLICATION NUMBER: US/09/546,238
;  CURRENT FILING DATE:  2000-04-10
;  PRIOR APPLICATION NUMBER:  US 60/033,151
;  PRIOR FILING DATE:  1996-12-13
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3032
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (97)..(2718)
US-09-546-238-1

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 3032;
  Best Local Similarity   85.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||| |||| |||| ||||||
Db    2219 GGCCGGGGCCGCCACAGCAG 2200


RESULT 13
PCT-US95-11684-1/c
; Sequence 1, Application PC/TUS9511684
;  GENERAL INFORMATION:
;    APPLICANT:  THE SCRIPPS RESEARCH INSTITUTE
;    TITLE OF INVENTION:  CYTOTACTIN DERIVATIVES THAT STIMULATE
;    TITLE OF INVENTION:  ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
;    TITLE OF INVENTION:  AND USING SAME
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  10666 North Torrey Pines Road, TPC 8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11684
;      FILING DATE:  14-SEP-1995
```

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;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/308,359
;      FILING DATE:  16-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Logan, April C.
;      REGISTRATION NUMBER:  33,950
;      REFERENCE/DOCKET NUMBER:  BEC0019P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7286 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  55..6654
;      OTHER INFORMATION:  /product= "cytotactin"
PCT-US95-11684-1

  Query Match             76.0%;  Score 15.2;  DB 5;  Length 7286;
  Best Local Similarity   85.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          ||||| ||  ||||||||||
Db   4359 GGCTGTGGAGGCCTCAGCAG 4340


RESULT 14
US-08-717-294-81/c
; Sequence 81, Application US/08717294
; Patent No. 6114148
;  GENERAL INFORMATION:
;    APPLICANT:  SEED, BRIAN
;    APPLICANT:  HAAS, JURGEN
;    TITLE OF INVENTION:  HIGH LEVEL EXPRESSION OF
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  110
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/717,294
;      FILING DATE:  20-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elbing, Karen L
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/345001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  81:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  105 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other
US-08-717-294-81

  Query Match             74.0%;  Score 14.8;  DB 3;  Length 105;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 GCTGGGGGCGCCTCAGCA 19
          ||||| ||||| ||||||
Db     77 GCTGGTGGCGCTTCAGCA 60


RESULT 15
US-08-487-113D-117
; Sequence 117, Application US/08487113D
; Patent No. 5837822
;  GENERAL INFORMATION:
;    APPLICANT:  Gallatin, W. Michael
;    APPLICANT:  Vazeux, Rosemay
;    TITLE OF INVENTION:  ICAM-Related Materials and Methods
;    NUMBER OF SEQUENCES:  120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,113D
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/286,754
;      FILING DATE:  05-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/102,852
;      FILING DATE:  05-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/009,266
;      FILING DATE:  22-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/894,061
;      FILING DATE:  05-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/889,724
;      FILING DATE:  26-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/827,689
;      FILING DATE:  27-JAN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5837822and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  32744
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  117:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1600 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
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US-08-487-113D-117

Query Match 74.0%; Score 14.8; DB 2; Length 1600;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3 CTGGGGGCGCCTCAGCAG 20
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Db    1299 CTGGGGGAGACTCAGCAG 1316
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Search completed: November 2, 2002, 17:08:40
Job time : 21.5455 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 16:08:01 ; Search time 719.455 Seconds
(without alignments)
375.200 Million cell updates/sec

Title: US-09-856-803-10
Perfect score: 20
Sequence: 1 ggctgggggcgcctcagcag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	427	9	AV647785	AV647785 AV647785
c 2	20	100.0	659	10	BI907636	BI907636 603065545
c 3	20	100.0	683	10	BG284879	BG284879 602409113
c 4	20	100.0	853	10	BI915042	BI915042 603177231
c 5	20	100.0	950	9	AL553611	AL553611 AL553611
c 6	20	100.0	995	10	BI519989	BI519989 603071783
c 7	18.4	92.0	406	10	BE245562	BE245562 TCBAP1E21
8	18.4	92.0	430	12	AQ539097	AQ539097 RPCI-11-3
c 9	18.4	92.0	646	10	BI911023	BI911023 603068746
10	18.4	92.0	710	10	BI765823	BI765823 603047436
11	18.4	92.0	777	10	BG704787	BG704787 602688415
c 12	18.4	92.0	848	10	BI767868	BI767868 603060993
c 13	18	90.0	161	10	C84644	C84644 C84644 oste
14	17.4	87.0	132	10	BF190014	BF190014 235965 MA
15	17.4	87.0	355	9	AA840344	AA840344 vw92a05.r
c 16	17.4	87.0	568	10	BE337782	BE337782 894048D05
c 17	17.4	87.0	610	10	BI722560	BI722560 1031062G0
c 18	17.4	87.0	642	10	BI527454	BI527454 1024081G0
c 19	17.4	87.0	668	10	BI719349	BI719349 1031042H1
c 20	17.4	87.0	675	10	BG845027	BG845027 1024008E0
c 21	17.4	87.0	684	10	BG845026	BG845026 1024008E0
c 22	17.4	87.0	732	10	BF864370	BF864370 963051B07
c 23	17.4	87.0	766	10	BF866118	BF866118 963066F01
24	17.4	87.0	888	10	BF536574	BF536574 602048741
c 25	17	85.0	240	9	BB386852	BB386852 BB386852
c 26	17	85.0	355	10	BE832452	BE832452 CM3-MT011
c 27	17	85.0	681	10	BI954411	BI954411 HVSMEm001
28	16.8	84.0	235	10	Z40858	Z40858 HSC2HC112 n
29	16.8	84.0	238	9	AW214864	AW214864 up02e10.y
30	16.8	84.0	269	10	BF375343	BF375343 QV4-ST023
31	16.8	84.0	298	9	AA910947	AA910947 ok85g07.s
32	16.8	84.0	320	9	AW214862	AW214862 up02e08.y
33	16.8	84.0	325	9	AA436399	AA436399 zv44b01.s
34	16.8	84.0	357	9	AA863430	AA863430 oh05c11.s
35	16.8	84.0	383	12	AQ212132	AQ212132 HS_3241_B
36	16.8	84.0	405	9	AW816455	AW816455 QV4-ST023
37	16.8	84.0	406	9	AW816371	AW816371 QV4-ST023
38	16.8	84.0	414	9	AA812309	AA812309 nr88c08.s
39	16.8	84.0	419	9	AI051840	AI051840 ox43g08.s
c 40	16.8	84.0	439	10	BF412089	BF412089 UI-R-BT1-
c 41	16.8	84.0	446	10	BM256430	BM256430 518797 MA
42	16.8	84.0	455	9	AW014907	AW014907 UI-H-BI0-
43	16.8	84.0	456	9	AA536122	AA536122 nj81f10.s
c 44	16.8	84.0	480	9	AA744145	AA744145 ny62d04.s
45	16.8	84.0	484	9	AA716195	AA716195 zh27e09.s

ALIGNMENTS

RESULT 1
AV647785/c
LOCUS AV647785 427 bp mRNA linear EST 15-JAN-2002
DEFINITION AV647785 GLC Homo sapiens cDNA clone GLCBCA03 3', mRNA sequence.
ACCESSION AV647785
VERSION AV647785.1 GI:9868799
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 427)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES Location/Qualifiers
source 1. .427
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCBCA03"
/clone_lib="GLC"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

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BASE COUNT       80 a    149 c    127 g     71 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 427;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          ||||||||||||||||||||
Db    168 GGCTGGGGGCGCCTCAGCAG 149


RESULT 2
BI907636/c
LOCUS       BI907636                659 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603065545F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214802 5',
            mRNA sequence.
ACCESSION   BI907636
VERSION     BI907636.1  GI:16170473
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 659)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11539  row: i  column: 11
            High quality sequence stop: 655.
FEATURES             Location/Qualifiers
     source          1. .659
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5214802"
                     /clone_lib="NIH_MGC_118"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
BASE COUNT      127 a    198 c    194 g    140 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 10;  Length 659;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          ||||||||||||||||||||
Db    150 GGCTGGGGGCGCCTCAGCAG 131


RESULT 3
BG284879/c
LOCUS       BG284879                683 bp    mRNA    linear   EST 21-FEB-2001
DEFINITION  602409113F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4538187 5',
            mRNA sequence.
ACCESSION   BG284879
VERSION     BG284879.1  GI:13036277
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 683)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10464  row: i  column: 04
            High quality sequence stop: 678.
FEATURES             Location/Qualifiers
     source          1. .683
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4538187"
                     /clone_lib="NIH_MGC_91"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.4 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      127 a    203 c    209 g    144 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 10;  Length 683;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          ||||||||||||||||||||
Db    190 GGCTGGGGGCGCCTCAGCAG 171


RESULT 4
BI915042/c
LOCUS       BI915042                853 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603177231F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5241774 5',
            mRNA sequence.
ACCESSION   BI915042
VERSION     BI915042.1  GI:16179135
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11609  row: m  column: 07
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            High quality sequence stop: 840.
FEATURES             Location/Qualifiers
     source          1. .853
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5241774"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      161 a    269 c    229 g    194 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 10;  Length 853;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db     161 GGCTGGGGGCGCCTCAGCAG 142


RESULT 5
AL553611/c
LOCUS       AL553611                950 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL553611 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI078YB15 5
            prime, mRNA sequence.
ACCESSION   AL553611
VERSION     AL553611.1  GI:12893606
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 950)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .950
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DI078YB15"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      183 a    291 c    262 g    210 t      4 others
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 950;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db     148 GGCTGGGGGCGCCTCAGCAG 129


RESULT 6
BI519989/c
LOCUS       BI519989                995 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603071783F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163669 5',
            mRNA sequence.
ACCESSION   BI519989
VERSION     BI519989.1  GI:15344781
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 995)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11406  row: f  column: 22
            High quality sequence start: 30
            High quality sequence stop: 687.
FEATURES             Location/Qualifiers
     source          1. .995
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5163669"
                     /clone_lib="NIH_MGC_119"
                     /tissue_type="medulla"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source normal medulla from
                     anonymous male age 27.  Library  is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.3 kb, insert size range
                     0.9-3 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 013. Note:
                     this is a NIH_MGC Library."
BASE COUNT      185 a    283 c    314 g    213 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 10;  Length 995;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db     575 GGCTGGGGGCGCCTCAGCAG 556


RESULT 7
BE245562/c
LOCUS       BE245562                406 bp    mRNA    linear   EST 03-OCT-2001
DEFINITION  TCBAP1E2132 Pediatric pre-B cell acute lymphoblastic leukemia
            Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2132, mRNA
            sequence.
ACCESSION   BE245562
VERSION     BE245562.1  GI:9097308
KEYWORDS    EST.
SOURCE      human.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 406)
  AUTHORS   Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D.
            , Bouck,J., Gibbs,R.A. and Margolin,J.F.
  TITLE     Pediatric Leukemia cDNA Sequencing Project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Dr. Judith F. Margolin
            Texas Children's Cancer Center and Human Genome Sequencing Center
            at Baylor College of Medicine
            1102 Bates, MC3-3320 Houston, TX 77030, USA
            Tel: 832-824-4536
            Fax: 832-825-4038
            Email: clones@txccc.org
            Citation: Carninci,P. and Hayashizaki,Y. High efficiency
            full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
            Seq primer: M13 primer.
FEATURES             Location/Qualifiers
     source          1. .406
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="TCBAP2132"
                     /clone_lib="Pediatric pre-B cell acute lymphoblastic
                     leukemia Baylor-HGSC project=TCBA"
                     /sex="male"
                     /tissue_type="leukopheresis"
                     /cell_type="pre-B cell"
                     /dev_stage="pediatric 2 years"
                     /lab_host="DH10B"
                     /note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
                     First strand cDNA was primed with an anchored
                     XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCCGCAGGAGGAG(T)VN
                     3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand
                     was primed with a BamH1-dC primer
                     [5'AGAGAGCTCGGATCCGCGGCCGCAATAATAATAAT(C) 3'].
                     Double-stranded cDNA was then digested with BamH1 and XhoI
                     and directionally cloned into the BamH1 and SalI sites of
                     lambda pSB vector. Library went through one round of
                     normalization. Library was constructed by Wei Yu at RIKEN
                     of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
                     Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M,
                     Schneider C, Hayashizaki Y, High efficiency selection of
                     full-length cDNA by improved biotinylated cap trapper.,
                     DNA Res 4: 1, 61-6, Feb 28, 1997)"
BASE COUNT       73 a    140 c    130 g     61 t      2 others
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 10;  Length 406;
  Best Local Similarity   95.0%;  Pred. No. 9.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          |||||||||||||||||| |
Db    194 GGCTGGGGGCGCCTCAGCGG 175


RESULT 8
AQ539097
LOCUS       AQ539097                 430 bp    DNA     linear   GSS 19-MAY-1999
DEFINITION  RPCI-11-324D17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-324D17
            , DNA sequence.
ACCESSION   AQ539097
VERSION     AQ539097.1  GI:4869736
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 430)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
            ,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: RPCI-11-324D17.TJ
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genetics (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .430
                     /organism="Homo sapiens"
                     /db_xref="GDB:7624120"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-324D17"
                     /clone_lib="RPCI-11"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
BASE COUNT       88 a    112 c    141 g     89 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 12;  Length 430;
  Best Local Similarity   95.0%;  Pred. No. 9.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          |||||||||||||||| ||||||
Db     42 GGCTGGGGGCGCCGCAGCAG 61


RESULT 9
BI911023/c
LOCUS       BI911023                 646 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603068746F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217922 5',
            mRNA sequence.
ACCESSION   BI911023
VERSION     BI911023.1  GI:16174544
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11547  row: k  column: 11
            High quality sequence stop: 643.
FEATURES             Location/Qualifiers
     source          1. .646
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5217922"
```

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                     /clone_lib="NIH_MGC_118"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated adult donors. Library is oligo-dT primed
                     and directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
BASE COUNT      114 a    209 c    189 g    134 t
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 10;  Length 646;
  Best Local Similarity  95.0%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          |||||||||||||||||| |
Db    162 GGCTGGGGGCGCCTCAGCGG 143


RESULT 10
BI765823
LOCUS       BI765823                710 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603047436F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5187512 5',
            mRNA sequence.
ACCESSION   BI765823
VERSION     BI765823.1  GI:15757401
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 710)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11468  row: h  column: 09
            High quality sequence start: 23
            High quality sequence stop: 682.
FEATURES             Location/Qualifiers
     source          1. .710
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5187512"
                     /clone_lib="NIH_MGC_116"
                     /lab_host="DH10B"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female. Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon cloning). Average insert size 1.4 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber (Invitrogen). Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
BASE COUNT      126 a    196 c    204 g    184 t
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 10;  Length 710;
  Best Local Similarity  95.0%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          |||||||||| ||||||||||
Db     72 GGCTGGGGGTGCCTCAGCAG 91


RESULT 11
BG704787
LOCUS       BG704787                777 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602688415F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4820931 5',
            mRNA sequence.
ACCESSION   BG704787
VERSION     BG704787.1  GI:13978473
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10726  row: n  column: 04
            High quality sequence stop: 725.
FEATURES             Location/Qualifiers
     source          1. .777
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4820931"
                     /clone_lib="NIH_MGC_95"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
                     size-selected for average insert size 2.5 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation). Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      179 a    205 c    231 g    162 t
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 10;  Length 777;
  Best Local Similarity  95.0%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          |||||||||||||| ||||
Db     69 GGCTGGGGGCGCCTCCGCAG 88


RESULT 12
BI767868/c
LOCUS       BI767868                848 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603060993F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5210231 5',
            mRNA sequence.
ACCESSION   BI767868
VERSION     BI767868.1  GI:15759446
```

```
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11527  row: j  column: 24
            High quality sequence stop: 845.
FEATURES             Location/Qualifiers
     source          1. .848
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5210231"
                     /clone_lib="NIH_MGC_122"
                     /lab_host="DH10B"
                     /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
                     anonymous pool of 24 week female lung, 16 week female
                     spleen, and 20-22 week male spleens.  Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon  cloning).  Average insert size 1.4 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was  constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking  code 026. Note:
                     this is a NIH_MGC Library."
BASE COUNT      157 a    265 c    230 g    195 t      1 others
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 10;  Length 848;
  Best Local Similarity   95.0%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           | ||||||||||||||||||||
Db     173 GACTGGGGGCGCCTCAGCAG 154


RESULT 13
C84644/c
LOCUS       C84644                   161 bp    mRNA    linear   EST 26-MAR-1999
DEFINITION  C84644 osteoclast subtracted library Oryctolagus cuniculus cDNA,
            mRNA sequence.
ACCESSION   C84644
VERSION     C84644.1  GI:4527904
KEYWORDS    EST.
SOURCE      rabbit.
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1  (bases 1 to 161)
  AUTHORS   Kobori,M., Ikeda,Y., Nara,H., Kato,M., Kumegawa,M., Nojima,H. and
            Kawashima,H.
  TITLE     Large scale isolation of osteoclast-specific genes by an improved
            method involving the preparation of a subtracted cDNA library
  JOURNAL   Genes Cells 3 (7), 459-475 (1998)
  MEDLINE   98424349
COMMENT     Contact: Kobori M
            Molecular Medicine Laboratories
            Institute for Drug Discovery Research,Yamanouchi Pharmaceutica
            21, Miyukigaoka, Tsukuba, Ibaraki 305, Japan
            Email: kobori@yamanouchi.co.jp
            PROJECT = 'OSG'.
FEATURES             Location/Qualifiers
     source          1. .161
                     /organism="Oryctolagus cuniculus"
                     /db_xref="taxon:9986"
                     /clone_lib="osteoclast subtracted library"
                     /tissue_type="long bone"
                     /cell_type="osteoclast"
                     /cell_line="primary"
                     /dev_stage="5 day-old"
BASE COUNT       34 a     52 c     36 g     38 t      1 others
ORIGIN

  Query Match             90.0%;  Score 18;  DB 10;  Length 161;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 GCTGGGGGCGCCTCAGCA 19
           ||||||||||||||||||
Db     132 GCTGGGGGCGCCTCAGCA 115


RESULT 14
BF190014
LOCUS       BF190014                 132 bp    mRNA    linear   EST 02-NOV-2000
DEFINITION  235965 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BF190014
VERSION     BF190014.1  GI:11073383
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 132)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 60  row: A  column: 6
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .132
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 2PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT       32 a     36 c     45 g     19 t
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 10;  Length 132;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCA 19
           |||||||||| ||||||||
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```
Db      34 GGCTGGGGGCTCCTCAGCA 52


RESULT 15
AA840344
LOCUS       AA840344                355 bp    mRNA    linear   EST 27-FEB-1998
DEFINITION  vw92a05.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
            IMAGE:1262384 5' similar to TR:Q14467 Q14467 MRNA ;, mRNA sequence.
ACCESSION   AA840344
VERSION     AA840344.1  GI:2916003
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 355)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:664936
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 310.
FEATURES             Location/Qualifiers
     source          1. .355
                     /organism="Mus musculus"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1262384"
                     /clone_lib="Stratagene mouse skin (#937313)"
                     /sex="females"
                     /tissue_type="whole skin"
                     /dev_stage="11 weeks old"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
                     ; Site_2: XhoI; Cloned unidirectionally.  Primer: Oligo
                     dT. Whole skin from 11 week old C57BL/6 female mice.
                     Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
                     adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor
                     sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT       81 a    107 c     95 g     72 t
ORIGIN

  Query Match            87.0%;  Score 17.4;  DB 9;  Length 355;
  Best Local Similarity  94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCA 19
           ||||||||  ||||||||||
Db     312 GGCTGGGGACGCCTCAGCA 330


Search completed: November  2, 2002, 17:57:24
Job time : 721.455 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 13:22:40 ; Search time 387.636 Seconds
(without alignments)
1079.699 Million cell updates/sec

Title: US-09-856-803-7
Perfect score: 20
Sequence: 1 ccccgccgtgggtccgcccg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
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23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	51	6	AX204248	AX204248 Sequence
2	20	100.0	230	6	AR164456	AR164456 Sequence
3	20	100.0	1970	9	HSBARR	X04827 Human mRNA
4	20	100.0	3451	6	AX022519	AX022519 Sequence
5	20	100.0	3451	6	AX022522	AX022522 Sequence
6	20	100.0	3451	6	AX332732	AX332732 Sequence
7	20	100.0	3451	6	AX334116	AX334116 Sequence
8	20	100.0	3451	9	HUMADRBR	M15169 Human beta-
9	20	100.0	133042	9	AC011354	AC011354 Homo sapi
10	20	100.0	134413	9	AC011334	AC011334 Homo sapi
11	18.4	92.0	2063	9	BC012481	BC012481 Homo sapi
12	18.4	92.0	2305	9	HSBAR	Y00106 Human gene
13	18.4	92.0	3451	6	AX022517	AX022517 Sequence
14	18.4	92.0	3451	6	AX022518	AX022518 Sequence
15	18.4	92.0	3451	6	AX022520	AX022520 Sequence
16	18.4	92.0	3451	6	AX022521	AX022521 Sequence
17	18.4	92.0	3451	6	AX022523	AX022523 Sequence
18	18.4	92.0	3458	9	HUMADRBRA	J02960 Human beta-
c 19	18	90.0	178000	1	SCO590463	AL590463 Streptomy
20	18	90.0	178073	1	SCO590464	AL590464 Streptomy
c 21	17.4	87.0	36816	2	AC109752	AC109752 Rattus no
c 22	17.4	87.0	49068	2	AC094344	AC094344 Rattus no
23	17.4	87.0	97834	2	AL354677	AL354677 Homo sapi
24	17.4	87.0	187865	2	AC015559	AC015559 Homo sapi
25	17.4	87.0	241098	2	AL662911	AL662911 Mus muscu
26	17	85.0	57108	2	AC099942	AC099942 Mus muscu
27	16.8	84.0	557	5	XELRGE12	K01371 X.laevis oo
c 28	16.8	84.0	599	8	AA1279460	AJ279460 Unidentif
29	16.8	84.0	3924	5	XELRGEE12	J00999 x.laevis ex
30	16.8	84.0	5477	1	CHBATP2OP	L08777 Chlorobium
31	16.8	84.0	5477	1	S56812	S56812 phospho eno
32	16.8	84.0	7517	1	AB022919	AB022919 Rhodopseu
33	16.8	84.0	7536	10	AB022047S1	AB022047 Mus muscu
34	16.8	84.0	7634	5	XL28SR	X59734 X.laevis 28
35	16.8	84.0	8153	5	XLRN01	X02995 Xenopus lae
c 36	16.8	84.0	71267	2	AC105963	AC105963 Mus muscu
37	16.8	84.0	85778	2	AC094467	AC094467 Rattus no
c 38	16.8	84.0	135044	9	AC006001	AC006001 Homo sapi
c 39	16.8	84.0	159315	2	AC095200	AC095200 Rattus no
c 40	16.8	84.0	167288	8	AC084831	AC084831 Oryza sat
c 41	16.8	84.0	172127	2	AC105872	AC105872 Rattus no
42	16.8	84.0	178652	2	AC103181	AC103181 Rattus no
43	16.8	84.0	187707	2	AC077693	AC077693 Oryza sat
44	16.8	84.0	230278	14	MCU68299	U68299 Mouse cytom
c 45	16.8	84.0	290221	2	AC102955	AC102955 Rattus no

ALIGNMENTS

RESULT 1
AX204248
LOCUS AX204248 51 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 354 from Patent WO0148245.
ACCESSION AX204248
VERSION AX204248.1 GI:15393760
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0148245-A 354 05-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
variation 26
/note="single nucleotide polymorphism

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                    Accession number cg43040273"
BASE COUNT        5 a      24 c      18 g       4 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db      8 CCCCGCCGTGGGTCCGCCCG 27


RESULT 2
AR164456
LOCUS       AR164456                 230 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 8 from patent US 6273893.
ACCESSION   AR164456
VERSION     AR164456.1  GI:16237489
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 230)
  AUTHORS   McAllen,J. III, Overaker,D.W. and Cooper,K.L.
  TITLE     Absorbable rivet/pin applier for use in surgical procedures
  JOURNAL   Patent: US 6273893-A 8 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .230
                     /organism="unknown"
BASE COUNT       42 a      91 c      70 g      27 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 230;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db    155 CCCCGCCGTGGGTCCGCCCG 174


RESULT 3
HSBARR
LOCUS       HSBARR                   1970 bp    mRNA    linear   PRI 12-SEP-1993
DEFINITION  Human mRNA for brain beta-adrenergic receptor.
ACCESSION   X04827
VERSION     X04827.1  GI:29372
KEYWORDS    beta-adrenergic receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1970)
  AUTHORS   Chung,F.Z., Lentes,K.U., Gocayne,J., Fitzgerald,M., Robinson,D.,
            Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
  TITLE     Cloning and sequence analysis of the human brain beta-adrenergic
            receptor. Evolutionary relationship to rodent and avian
            beta-receptors and porcine muscarinic receptors
  JOURNAL   FEBS Lett. 211 (2), 200-206 (1987)
  MEDLINE   87105974
REFERENCE   2  (bases 1 to 1970)
  AUTHORS   Kerlavage,A.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-SEP-1987)
COMMENT     substantial corrections are reported in [2]
            Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
FEATURES             Location/Qualifiers
     source          1. .1970
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="neonatal human brain stem"
     CDS             178. .1419
                     /note="beta-adrenergic receptor (AA 1-413)"
                     /codon_start=1
                     /protein_id="CAA28511.1"
                     /db_xref="GI:29373"
                     /db_xref="SWISS-PROT:P07550"
                     /translation="MGQPGNGSAFLLAPNGSHAPDHDVTQERDEVWVVGMGIVMSLIV
                     LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
                     NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                     IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                     AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                     TVPSDNIDSQGRNCSTNDSLL"
     misc_feature    794. .799
                     /note="pot. glucocorticoid-responsive element"
     misc_feature    965. .970
                     /note="pot. glucocorticoid-responsive element"
     misc_feature    1459. .1464
                     /note="pot. glucocorticoid-responsive element"
     misc_feature    1491. .1496
                     /note="pot. polyA signal"
     misc_feature    1502. .1507
                     /note="pot. polyA signal"
     misc_feature    1952. .1957
                     /note="pot. polyA signal"
     polyA_site      1970
                     /note="polyA site"
BASE COUNT      459 a     508 c     482 g     521 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 1970;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db    113 CCCCGCCGTGGGTCCGCCCG 132


RESULT 4
AX022519
LOCUS       AX022519                 3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 3 from Patent WO9937761.
ACCESSION   AX022519
VERSION     AX022519.1  GI:10046118
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 3 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      789 a     872 c     897 g     893 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db   1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 5
```

```
AX022522
LOCUS       AX022522               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 6 from Patent WO9937761.
ACCESSION   AX022522
VERSION     AX022522.1  GI:10046121
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 6 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      789 a    873 c    897 g    892 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db   1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 6
AX332732
LOCUS       AX332732               3451 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 3241 from Patent WO0194629.
ACCESSION   AX332732
VERSION     AX332732.1  GI:18123366
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 3241 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      790 a    873 c    895 g    893 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db   1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 7
AX334116
LOCUS       AX334116               3451 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 4625 from Patent WO0194629.
ACCESSION   AX334116
VERSION     AX334116.1  GI:18124835
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 4625 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      790 a    873 c    895 g    893 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db   1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 8
HUMADRBR
LOCUS       HUMADRBR               3451 bp    mRNA    linear   PRI 13-FEB-1996
DEFINITION  Human beta-2-adrenergic receptor mRNA, complete cds.
ACCESSION   M15169 J02728 M16106
VERSION     M15169.1  GI:178201
KEYWORDS    adrenergic receptor.
SOURCE      Homo sapiens (clone: pTF.) (tissue library: Evan Sadler) placenta
            cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Kobilka,B.K., Frielle,T., Dohlman,H.G., Bolanowski,M.A.,
            Dixon,R.A., Keller,P., Caron,M.G. and Lefkowitz,R.J.
  TITLE     Delineation of the intronless nature of the genes for the human and
            hamster beta 2-adrenergic receptor and their putative promoter
            regions
  JOURNAL   J. Biol. Chem. 262 (15), 7321-7327 (1987)
  MEDLINE   87222338
REFERENCE   2  (bases 1399 to 1985)
  AUTHORS   Kobilka,B.K., Dixon,R.A., Frielle,T., Dohlman,H.G.,
            Bolanowski,M.A., Sigal,I.S., Yang-Feng,T.L., Francke,U., Caron,M.G.
            and Lefkowitz,R.J.
  TITLE     cDNA for the human beta 2-adrenergic receptor: a protein with
            multiple membrane-spanning domains and encoded by a gene whose
            chromosomal location is shared with that of the receptor for
            platelet-derived growth factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (1), 46-50 (1987)
  MEDLINE   87092393
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="5q31-q32"
                     /clone="pTF."
                     /tissue_type="placenta"
                     /tissue_lib="Evan Sadler"
     mRNA            1369. .3383
                     /gene="ADRB2"
                     /note="b-2-adr mRNA (alt.); G00-120-541"
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                     /note="b-2-adr mRNA (alt.); G00-120-541"
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     mRNA            1379. .3383
                     /gene="ADRB2"
                     /note="b-2-adr mRNA (alt.); G00-120-541"
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                     /gene="ADRB2"
                     /note="b-2-adr mRNA (alt.); G00-120-541"
     CDS             1487. .1546
                     /gene="ADRB2"
                     /note="putative"
                     /codon_start=1
                     /protein_id="AAA88014.1"
                     /db_xref="GI:560761"
                     /db_xref="GDB:G00-120-541"
                     /translation="MRLPGVRSRPAEPRRGSAR"
     CDS             1588. .2829
                     /gene="ADRB2"
                     /codon_start=1
                     /product="beta-2 adrenergic receptor"
                     /protein_id="AAA88015.1"
                     /db_xref="GI:178202"
                     /db_xref="GDB:G00-120-541"
                     /translation="MGQPGNGSAFLLAPNRSHAPDHDVTQQRDEVWVVGMGIVMSLIV
                     LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
                     NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                     IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                     AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                     TVPSDNIDSQGRNCSTNDSLL"
BASE COUNT      790 a    873 c    895 g    893 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 9;  Length 3451;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db   1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 9
AC011354
LOCUS       AC011354              133042 bp    DNA     linear   PRI 27-JUN-2001
DEFINITION  Homo sapiens chromosome 5 clone CTC-354F19, complete sequence.
ACCESSION   AC011354
VERSION     AC011354.4  GI:14572125
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 133042)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 133042)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 133042)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jun 27, 2001 this sequence version replaced gi:13699555.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.9% of Sequence;
            Estimated Total Number of Errors is 0.1.
FEATURES             Location/Qualifiers
     source          1. .133042
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTC-354F19"
BASE COUNT    40170 a  26580 c  25753 g  40539 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 9;  Length 133042;
  Best Local Similarity  100.0%;  Pred. No. 46;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db 127722 CCCCGCCGTGGGTCCGCCCG 127741


RESULT 10
AC011334
LOCUS       AC011334              134413 bp    DNA     linear   PRI 27-NOV-2001
DEFINITION  Homo sapiens chromosome 5 clone CTC-235N17, complete sequence.
ACCESSION   AC011334
VERSION     AC011334.5  GI:17105283
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 134413)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 134413)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 134413)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Nov 27, 2001 this sequence version replaced gi:12830127.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 100% of Sequence;
            Estimated Total Number of Errors is 0.
FEATURES             Location/Qualifiers
     source          1. .134413
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTC-235N17"
BASE COUNT    40269 a  28043 c  27434 g  38667 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 46;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db  54688 CCCCGCCGTGGGTCCGCCCG 54707


RESULT 11
BC012481
LOCUS       BC012481              2063 bp    mRNA    linear   PRI 20-AUG-2001
DEFINITION  Homo sapiens, Similar to adrenergic, beta-2-, receptor, surface,
            clone MGC:21367 IMAGE:4538187, mRNA, complete cds.
```

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ACCESSION   BC012481
VERSION     BC012481.1  GI:15214693
KEYWORDS    MGC.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2063)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-AUG-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: villalon@bcm.tmc.edu.
            Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
            A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
            Muzny,D.M., Gibbs,R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 28 Row: k Column: 6
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 178203.
FEATURES             Location/Qualifiers
     source          1. .2063
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="MGC:21367 IMAGE:4538187"
                     /tissue_type="Prostate, adenocarcinoma."
                     /clone_lib="NIH_MGC_91"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             222. .1463
                     /codon_start=1
                     /product="Similar to adrenergic, beta-2-, receptor,
                     surface"
                     /protein_id="AAH12481.1"
                     /db_xref="GI:15214694"
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                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                     IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                     AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                     TVPSDNIDSPGRNCSTNDSLL"
BASE COUNT      512 a    522 c    498 g    531 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 9;  Length 2063;
  Best Local Similarity   95.0%;  Pred. No. 6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||||||||||||||| |
Db    157 CCCCGCCGTGGGTCCGCCTG 176


RESULT 12
HSBAR
LOCUS       HSBAR                   2305 bp    DNA     linear   PRI 12-SEP-1993
DEFINITION  Human gene for beta-adrenergic receptor (beta-2 subtype).
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ACCESSION   Y00106
VERSION     Y00106.1  GI:29370
KEYWORDS    beta-adrenergic receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2305)
  AUTHORS   Schofield,P.R., Rhee,L.M. and Peralta,E.G.
  TITLE     Primary structure of the human beta-adrenergic receptor gene
  JOURNAL   Nucleic Acids Res. 15 (8), 3636 (1987)
  MEDLINE   87203400
REFERENCE   2  (bases 1 to 2305)
  AUTHORS   Schofield,P.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-OCT-1987)
FEATURES             Location/Qualifiers
     source          1. .2305
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="lambdahbetaAR17"
                     /clone_lib="Maniatis human"
     CDS             794. .2035
                     /note="beta-adrenergic receptor (AA 1 - 413)"
                     /codon_start=1
                     /protein_id="CAA68289.1"
                     /db_xref="GI:29371"
                     /db_xref="SWISS-PROT:P07550"
                     /translation="MGQPGNGSAFLLAPNRSHAPDHDVTQQRDEVWVVGMGIVMSLIV
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                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
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     misc_feature    809. .817
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                     /note="N-linked glycosylation site"
     misc_feature    896. .967
                     /note="membrane spanning domain I"
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                     /note="membrane spanning domain II"
     misc_feature    1114. .1180
                     /note="membrane spanning domain III"
     misc_feature    1247. .1315
                     /note="membrane spanning domain IV"
     misc_feature    1385. .1450
                     /note="membrane spanning domain V"
     misc_feature    1616. .1687
                     /note="membrane spanning domain VI"
     misc_feature    1712. .1774
                     /note="membrane spanning domain VII"
BASE COUNT      495 a    616 c    649 g    545 t
ORIGIN

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  Best Local Similarity   95.0%;  Pred. No. 5.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
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Db    729 CCCCGCCGTGGGTCCGCCTG 748


RESULT 13
AX022517
LOCUS       AX022517                3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9937761.
ACCESSION   AX022517
VERSION     AX022517.1  GI:10046115
KEYWORDS    .
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SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 1 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      794 a    871 c    892 g    894 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 3451;
  Best Local Similarity   95.0%;  Pred. No. 5.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||||||||||||||| |
Db   1523 CCCCGCCGTGGGTCCGCCTG 1542


RESULT 14
AX022518
LOCUS       AX022518               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9937761.
ACCESSION   AX022518
VERSION     AX022518.1  GI:10046116
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 2 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      790 a    872 c    895 g    894 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 3451;
  Best Local Similarity   95.0%;  Pred. No. 5.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||||||||||||||| |
Db   1523 CCCCGCCGTGGGTCCGCCTG 1542


RESULT 15
AX022520
LOCUS       AX022520               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from Patent WO9937761.
ACCESSION   AX022520
VERSION     AX022520.1  GI:10046119
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 4 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      789 a    872 c    896 g    894 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 3451;
  Best Local Similarity   95.0%;  Pred. No. 5.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          |||||||||||||||||| |
Db   1523 CCCCGCCGTGGGTCCGCCTG 1542


Search completed: November 2, 2002, 16:50:24
Job time : 416.636 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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Title: US-09-856-803-10
Perfect score: 20
Sequence: 1 ggctgggggcgcctcagcag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	2063	9	BC012481	BC012481 Homo sapi
c 2	20	100.0	2305	9	HSBAR	Y00106 Human gene
c 3	20	100.0	3451	6	AX022517	AX022517 Sequence
c 4	20	100.0	3451	6	AX022518	AX022518 Sequence
c 5	20	100.0	3451	6	AX022520	AX022520 Sequence
c 6	20	100.0	3451	6	AX022521	AX022521 Sequence
c 7	20	100.0	3451	6	AX022523	AX022523 Sequence
c 8	20	100.0	3458	9	HUMADRBRA	J02960 Human beta-
c 9	18.4	92.0	51	6	AX204248	AX204248 Sequence
c 10	18.4	92.0	230	6	AR164456	AR164456 Sequence
c 11	18.4	92.0	1970	9	HSBARR	X04827 Human mRNA
c 12	18.4	92.0	3451	6	AX022519	AX022519 Sequence
c 13	18.4	92.0	3451	6	AX022522	AX022522 Sequence
c 14	18.4	92.0	3451	6	AX332732	AX332732 Sequence
c 15	18.4	92.0	3451	6	AX334116	AX334116 Sequence
c 16	18.4	92.0	3451	9	HUMADRBR	M15169 Human beta-
c 17	18.4	92.0	133042	9	AC011354	AC011354 Homo sapi
c 18	18.4	92.0	134413	9	AC011334	AC011334 Homo sapi
c 19	18.4	92.0	163494	2	AC016964	AC016964 Homo sapi
20	18.4	92.0	170669	9	AC007907	AC007907 Homo sapi
c 21	18.4	92.0	171488	2	AC096970	AC096970 Homo sapi
22	18.4	92.0	175483	2	AC018553	AC018553 Homo sapi
c 23	18.4	92.0	190506	2	AC068990	AC068990 Homo sapi
24	18	90.0	142239	2	AC027635	AC027635 Homo sapi
25	17.4	87.0	2629	2	AC092861	AC092861 Homo sapi
26	17.4	87.0	4078	10	AF334144	AF334144 Mus muscu
c 27	17.4	87.0	65144	2	AC090665	AC090665 Homo sapi
c 28	17.4	87.0	76825	2	AL159165	AL159165 Homo sapi
29	17.4	87.0	119555	9	AL353790	AL353790 Human DNA
c 30	17.4	87.0	125057	9	AL133419	AL133419 Human DNA
c 31	17.4	87.0	147712	9	AC011299	AC011299 Homo sapi
32	17.4	87.0	154467	2	AC022566	AC022566 Homo sapi
33	17.4	87.0	165900	9	AC005552	AC005552 Homo sapi
c 34	17.4	87.0	167362	2	AC107312	AC107312 Homo sapi
35	17.4	87.0	198246	2	AC017090	AC017090 Homo sapi
36	17.4	87.0	220848	2	AC091579	AC091579 Homo sapi
37	17	85.0	6108	4	AF217204	AF217204 Canis fam
38	16.8	84.0	1222	9	F327658S01	AF327658 Homo sapi
c 39	16.8	84.0	1457	10	BC022726	BC022726 Mus muscu
c 40	16.8	84.0	1926	6	AR065785	AR065785 Sequence
c 41	16.8	84.0	1926	6	AR073875	AR073875 Sequence
c 42	16.8	84.0	2033	9	HSA312322	AJ312322 Homo sapi
c 43	16.8	84.0	2066	5	CHKMYBPH	L05605 Chicken myo
c 44	16.8	84.0	2257	3	DAU23167	U23167 Drosophila
c 45	16.8	84.0	2562	9	HSA312321	AJ312321 Homo sapi

ALIGNMENTS

RESULT 1
BC012481/c
LOCUS BC012481 2063 bp mRNA linear PRI 20-AUG-2001
DEFINITION Homo sapiens, Similar to adrenergic, beta-2-, receptor, surface, clone MGC:21367 IMAGE:4538187, mRNA, complete cds.
ACCESSION BC012481
VERSION BC012481.1 GI:15214693
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2063)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP

```
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: villalon@bcm.tmc.edu.
            Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
            A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
            Muzny,D.M., Gibbs,R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 28 Row: k Column: 6
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 178203.
FEATURES              Location/Qualifiers
     source           1. .2063
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="MGC:21367 IMAGE:4538187"
                      /tissue_type="Prostate, adenocarcinoma."
                      /clone_lib="NIH_MGC_91"
                      /lab_host="DH10B"
                      /note="Vector: pCMV-SPORT6"
     CDS              222. .1463
                      /codon_start=1
                      /product="Similar to adrenergic, beta-2-, receptor,
                      surface"
                      /protein_id="AAH12481.1"
                      /db_xref="GI:15214694"
                      /translation="MGQPGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
                      LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
                      NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                      SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                      YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                      IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                      AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                      TVPSDNIDSPGRNCSTNDSLL"
BASE COUNT      512 a    522 c    498 g    531 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 9;  Length 2063;
  Best Local Similarity  100.0%;  Pred. No. 19;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          ||||||||||||||||||||
Db    193 GGCTGGGGGCGCCTCAGCAG 174


RESULT 2
HSBAR/c
LOCUS       HSBAR                   2305 bp    DNA     linear   PRI 12-SEP-1993
DEFINITION  Human gene for beta-adrenergic receptor (beta-2 subtype).
ACCESSION   Y00106
VERSION     Y00106.1  GI:29370
KEYWORDS    beta-adrenergic receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2305)
  AUTHORS   Schofield,P.R., Rhee,L.M. and Peralta,E.G.
  TITLE     Primary structure of the human beta-adrenergic receptor gene
  JOURNAL   Nucleic Acids Res. 15 (8), 3636 (1987)
  MEDLINE   87203400
REFERENCE   2  (bases 1 to 2305)
  AUTHORS   Schofield,P.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-OCT-1987)
FEATURES              Location/Qualifiers
     source           1. .2305
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="lambdahbetaAR17"
                      /clone_lib="Maniatis human"
     CDS              794. .2035
                      /note="beta-adrenergic receptor (AA 1 - 413)"
                      /codon_start=1
                      /protein_id="CAA68289.1"
                      /db_xref="GI:29371"
                      /db_xref="SWISS-PROT:P07550"
                      /translation="MGQPGNGSAFLLAPNRSHAPDHDVTQQRDEVWVVGMGIVMSLIV
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                      NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                      SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                      YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                      IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                      AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                      TVPSDNIDSQGRNCSTNDSLL"
     misc_feature     809. .817
                      /note="N-linked glycosylation site"
     misc_feature     836. .844
                      /note="N-linked glycosylation site"
     misc_feature     896. .967
                      /note="membrane spanning domain I"
     misc_feature     1007. .1078
                      /note="membrane spanning domain II"
     misc_feature     1114. .1180
                      /note="membrane spanning domain III"
     misc_feature     1247. .1315
                      /note="membrane spanning domain IV"
     misc_feature     1385. .1450
                      /note="membrane spanning domain V"
     misc_feature     1616. .1687
                      /note="membrane spanning domain VI"
     misc_feature     1712. .1774
                      /note="membrane spanning domain VII"
BASE COUNT      495 a    616 c    649 g    545 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 9;  Length 2305;
  Best Local Similarity  100.0%;  Pred. No. 19;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
          ||||||||||||||||||||
Db    765 GGCTGGGGGCGCCTCAGCAG 746


RESULT 3
AX022517/c
LOCUS       AX022517                3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9937761.
ACCESSION   AX022517
VERSION     AX022517.1  GI:10046115
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 1 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES              Location/Qualifiers
     source           1. .3451
                      /organism="unidentified"
                      /db_xref="taxon:32644"
BASE COUNT      794 a    871 c    892 g    894 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 3451;
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  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCAG 1540


RESULT 4
AX022518/c
LOCUS       AX022518               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9937761.
ACCESSION   AX022518
VERSION     AX022518.1  GI:10046116
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 2 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      790 a    872 c    895 g    894 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCAG 1540


RESULT 5
AX022520/c
LOCUS       AX022520               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from Patent WO9937761.
ACCESSION   AX022520
VERSION     AX022520.1  GI:10046119
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 4 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      789 a    872 c    896 g    894 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCAG 1540


RESULT 6
AX022521/c
LOCUS       AX022521               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 5 from Patent WO9937761.
ACCESSION   AX022521
VERSION     AX022521.1  GI:10046120
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 5 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      790 a    872 c    895 g    894 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCAG 1540


RESULT 7
AX022523/c
LOCUS       AX022523               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 7 from Patent WO9937761.
ACCESSION   AX022523
VERSION     AX022523.1  GI:10046122
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 7 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      789 a    872 c    896 g    894 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCAG 1540


RESULT 8
HUMADRBRA/c
LOCUS       HUMADRBRA              3458 bp    DNA     linear   PRI 13-FEB-1996
DEFINITION  Human beta-2-adrenergic receptor gene, complete cds.
ACCESSION   J02960
VERSION     J02960.1  GI:178203
```

```
KEYWORDS    adrenergic receptor; beta-2 adrenergic receptor.
SOURCE      Homo sapiens (clone: H-beta-R-[9,10,11].) epidermis DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3458)
  AUTHORS   Emorine,L.J., Marullo,S., Delavier-Klutchko,C., Kaveri,S.V.,
            Durieu-Trautmann,O. and Strosberg,A.D.
  TITLE     Structure of the gene for human beta 2-adrenergic receptor:
            expression and promoter characterization
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (20), 6995-6999 (1987)
  MEDLINE   88041037
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by L.J.Emorine, 25-AUG-1987.
FEATURES             Location/Qualifiers
     source          1. .3458
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="5q31-q32"
                     /clone="H-beta-R-[9,10,11]."
                     /cell_line="A431"
                     /tissue_type="epidermis"
     CDS             277. .1032
                     /note="ORF; putative"
                     /codon_start=1
                     /product="unknown protein"
                     /protein_id="AAA88016.1"
                     /db_xref="GI:560762"
                     /translation="MFEREYTGLPGVCWEGSIISARVRQVRSTQMETSVSVSLWMPPS
                     QRVFTFCVCHHVFVLLGASVFVSGRVSVLDRGDFVPDGFCVRARASVHVGELGGCVSV
                     SMAVVRYKSEHVCQGVFVPVCACLGGHSRFLPNVGQCRCAALCLETSSRAGAQGRQVA
                     ATEEPKAPGLAGKHTTSSFSPLGPARVAGKQWWPALQGAVGPRPGQPQEKEGEGRGGK
                     GEECLAPSRLPACHWPKVPVRHGEGSSPKVLCT"
     mRNA            1045. .3057
                     /note="beta-2-adrenergic receptor mRNA (alt.)"
     mRNA            1055. .3057
                     /note="beta-2-adrenergic receptor mRNA (alt.)"
     mRNA            1064. .3057
                     /note="beta-2-adrenergic receptor mRNA (alt.)"
     gene            1264. .2505
                     /gene="ADRB2"
     CDS             1264. .2505
                     /gene="ADRB2"
                     /codon_start=1
                     /product="beta-2 adrenergic receptor"
                     /protein_id="AAA88017.1"
                     /db_xref="GI:178204"
                     /db_xref="GDB:G00-120-541"
                     /translation="MGQPGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
                     LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
                     NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                     IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                     AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                     TVPSDNIDSQGRNCSTNDSLL"
BASE COUNT      777 a    890 c    886 g    905 t
ORIGIN      1 bp upstream of EcoRI site; chromosome 5q31-q32.
```

Query Match 100.0%; Score 20; DB 9; Length 3458;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           ||||||||||||||||||||
Db    1235 GGCTGGGGGCGCCTCAGCAG 1216
```

```
RESULT 9
AX204248/c
LOCUS       AX204248                  51 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 354 from Patent WO0148245.
ACCESSION   AX204248
VERSION     AX204248.1  GI:15393760
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0148245-A 354 05-JUL-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     variation       26
                     /note="single nucleotide polymorphism
                     Accession number cg43040273"
BASE COUNT        5 a     24 c     18 g      4 t
ORIGIN
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Query Match 92.0%; Score 18.4; DB 6; Length 51;
Best Local Similarity 95.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           |||||||||||||||||| |
Db      44 GGCTGGGGGCGCCTCAGCGG 25
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```
RESULT 10
AR164456/c
LOCUS       AR164456                  230 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 8 from patent US 6273893.
ACCESSION   AR164456
VERSION     AR164456.1  GI:16237489
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 230)
  AUTHORS   McAllen,J. III, Overaker,D.W. and Cooper,K.L.
  TITLE     Absorbable rivet/pin applier for use in surgical procedures
  JOURNAL   Patent: US 6273893-A 8 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .230
                     /organism="unknown"
BASE COUNT       42 a     91 c     70 g     27 t
ORIGIN
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Query Match 92.0%; Score 18.4; DB 6; Length 230;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 GGCTGGGGGCGCCTCAGCAG 20
           |||||||||||||||||| |
Db     191 GGCTGGGGGCGCCTCAGCGG 172
```

```
RESULT 11
HSBARR/c
LOCUS       HSBARR                   1970 bp    mRNA    linear   PRI 12-SEP-1993
DEFINITION  Human mRNA for brain beta-adrenergic receptor.
ACCESSION   X04827
VERSION     X04827.1  GI:29372
KEYWORDS    beta-adrenergic receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1970)
  AUTHORS   Chung,F.Z., Lentes,K.U., Gocayne,J., Fitzgerald,M., Robinson,D.,
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            Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
  TITLE     Cloning and sequence analysis of the human brain beta-adrenergic
            receptor. Evolutionary relationship to rodent and avian
            beta-receptors and porcine muscarinic receptors
  JOURNAL   FEBS Lett. 211 (2), 200-206 (1987)
  MEDLINE   87105974
REFERENCE   2  (bases 1 to 1970)
  AUTHORS   Kerlavage,A.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-SEP-1987)
COMMENT     substantial corrections are reported in [2]
            Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
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                     /db_xref="SWISS-PROT:P07550"
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                     /note="pot. glucocorticoid-responsive element"
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RESULT 12
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LOCUS       AX022519               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 3 from Patent WO9937761.
ACCESSION   AX022519
VERSION     AX022519.1  GI:10046118
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 3 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
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  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db    1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 13
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LOCUS       AX022522               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 6 from Patent WO9937761.
ACCESSION   AX022522
VERSION     AX022522.1  GI:10046121
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 6 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
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BASE COUNT      789 a    873 c    897 g    892 t
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  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db    1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 14
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LOCUS       AX332732               3451 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 3241 from Patent WO0194629.
ACCESSION   AX332732
VERSION     AX332732.1  GI:18123366
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 3241 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
BASE COUNT      790 a    873 c    895 g    893 t
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ORIGIN

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Db   1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 15
AX334116/c
LOCUS       AX334116               3451 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 4625 from Patent WO0194629.
ACCESSION   AX334116
VERSION     AX334116.1  GI:18124835
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 4625 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .3451
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BASE COUNT      790 a    873 c    895 g    893 t
ORIGIN

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  Best Local Similarity  95.0%;  Pred. No. 1.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCAG 20
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Db   1559 GGCTGGGGGCGCCTCAGCGG 1540


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GenCore version 5.1.3

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Perfect score: 20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	51	6	AX204248	AX204248 Sequence
c 2	20	100.0	230	6	AR164456	AR164456 Sequence
c 3	20	100.0	1970	9	HSBARR	X04827 Human mRNA
c 4	20	100.0	3451	6	AX022519	AX022519 Sequence
c 5	20	100.0	3451	6	AX022522	AX022522 Sequence
c 6	20	100.0	3451	6	AX332732	AX332732 Sequence
c 7	20	100.0	3451	6	AX334116	AX334116 Sequence
c 8	20	100.0	3451	9	HUMADRBR	M15169 Human beta-
c 9	20	100.0	133042	9	AC011354	AC011354 Homo sapi
c 10	20	100.0	134413	9	AC011334	AC011334 Homo sapi
11	19	95.0	142239	2	AC027635	AC027635 Homo sapi
c 12	18.4	92.0	2063	9	BC012481	BC012481 Homo sapi
c 13	18.4	92.0	2305	9	HSBAR	Y00106 Human gene
c 14	18.4	92.0	3451	6	AX022517	AX022517 Sequence
c 15	18.4	92.0	3451	6	AX022518	AX022518 Sequence
c 16	18.4	92.0	3451	6	AX022520	AX022520 Sequence
c 17	18.4	92.0	3451	6	AX022521	AX022521 Sequence
c 18	18.4	92.0	3451	6	AX022523	AX022523 Sequence
c 19	18.4	92.0	3458	9	HUMADRBRA	J02960 Human beta-
20	18.4	92.0	149515	2	AC012615	AC012615 Homo sapi
21	17.4	87.0	6108	4	AF217204	AF217204 Canis fam
22	17.4	87.0	153938	2	AC080050	AC080050 Homo sapi
c 23	17.4	87.0	158983	2	AC020598	AC020598 Homo sapi
c 24	17.4	87.0	170220	9	AC012486	AC012486 Homo sapi
25	17.4	87.0	197008	2	AC092171	AC092171 Homo sapi
26	17	85.0	2629	2	AC092861	AC092861 Homo sapi
c 27	17	85.0	65144	2	AC090665	AC090665 Homo sapi
c 28	17	85.0	76825	2	AL159165	AL159165 Homo sapi
c 29	17	85.0	125057	9	AL133419	AL133419 Human DNA
c 30	17	85.0	147712	9	AC011299	AC011299 Homo sapi
31	17	85.0	154467	2	AC022566	AC022566 Homo sapi
c 32	17	85.0	167362	2	AC107312	AC107312 Homo sapi
33	17	85.0	198246	2	AC017090	AC017090 Homo sapi
c 34	16.8	84.0	469	9	HSA323085	AJ323085 Homo sapi
35	16.8	84.0	901	6	AX014224	AX014224 Sequence
36	16.8	84.0	1184	6	AX337830	AX337830 Sequence
37	16.8	84.0	1184	9	HSCHYPRO	X71877 H.sapiens m
38	16.8	84.0	2022	1	RHMPMIA	M96584 Rhizobium m
c 39	16.8	84.0	2078	9	BC000099	BC000099 Homo sapi
c 40	16.8	84.0	2102	9	AY046538	AY046538 Homo sapi
c 41	16.8	84.0	3106	9	AF006751	AF006751 Homo sapi
c 42	16.8	84.0	5468	9	AB037819	AB037819 Homo sapi
43	16.8	84.0	13863	9	HSPROSCHY	X71874 H.sapiens g
c 44	16.8	84.0	34068	2	HS312E8	AL032819 Homo sapi
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ALIGNMENTS

RESULT 1
AX204248/c
LOCUS AX204248 51 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 354 from Patent WO0148245.
ACCESSION AX204248
VERSION AX204248.1 GI:15393760
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0148245-A 354 05-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1. .51
/organism="Homo sapiens"
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 44 GGCTGGGGGCGCCTCAGCGG 25

RESULT 2
AR164456/c
LOCUS AR164456 230 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6273893.
ACCESSION AR164456
VERSION AR164456.1 GI:16237489
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 230)
AUTHORS McAllen,J. III, Overaker,D.W. and Cooper,K.L.
TITLE Absorbable rivet/pin applier for use in surgical procedures
JOURNAL Patent: US 6273893-A 8 14-AUG-2001;
FEATURES Location/Qualifiers
source 1. .230
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BASE COUNT 42 a 91 c 70 g 27 t
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Db 191 GGCTGGGGGCGCCTCAGCGG 172

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LOCUS HSBARR 1970 bp mRNA linear PRI 12-SEP-1993
DEFINITION Human mRNA for brain beta-adrenergic receptor.
ACCESSION X04827
VERSION X04827.1 GI:29372
KEYWORDS beta-adrenergic receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1970)
AUTHORS Chung,F.Z., Lentes,K.U., Gocayne,J., Fitzgerald,M., Robinson,D.,
Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
TITLE Cloning and sequence analysis of the human brain beta-adrenergic
receptor. Evolutionary relationship to rodent and avian
beta-receptors and porcine muscarinic receptors
JOURNAL FEBS Lett. 211 (2), 200-206 (1987)
MEDLINE 87105974
REFERENCE 2 (bases 1 to 1970)
AUTHORS Kerlavage,A.R.
TITLE Direct Submission
JOURNAL Submitted (22-SEP-1987)
COMMENT substantial corrections are reported in [2]
Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
FEATURES Location/Qualifiers
source 1. .1970
/organism="Homo sapiens"
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/note="polyA site"
BASE COUNT 459 a 508 c 482 g 521 t
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 149 GGCTGGGGGCGCCTCAGCGG 130

RESULT 4
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LOCUS AX022519 3451 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 3 from Patent WO9937761.
ACCESSION AX022519
VERSION AX022519.1 GI:10046118
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 3451)
AUTHORS Hoehe,M., Koepke,K. and Timmermann,B.
TITLE Novel sequence variants of the human beta2-adrenergic receptor gene
and use thereof
JOURNAL Patent: WO 9937761-A 3 29-JUL-1999;
HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES Location/Qualifiers
source 1. .3451
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BASE COUNT 789 a 872 c 897 g 893 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGGGCGCCTCAGCGG 20
||||||||||||||||||||
Db 1559 GGCTGGGGGCGCCTCAGCGG 1540

RESULT 5

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AX022522/c
LOCUS       AX022522               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 6 from Patent WO9937761.
ACCESSION   AX022522
VERSION     AX022522.1  GI:10046121
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 6 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      789 a    873 c    897 g    892 t
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
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Db    1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 6
AX332732/c
LOCUS       AX332732               3451 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 3241 from Patent WO0194629.
ACCESSION   AX332732
VERSION     AX332732.1  GI:18123366
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 3241 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .3451
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 77;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 7
AX334116/c
LOCUS       AX334116               3451 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 4625 from Patent WO0194629.
ACCESSION   AX334116
VERSION     AX334116.1  GI:18124835
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 4625 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
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BASE COUNT      790 a    873 c    895 g    893 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity  100.0%;  Pred. No. 77;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 8
HUMADRBR/c
LOCUS       HUMADRBR               3451 bp    mRNA    linear   PRI 13-FEB-1996
DEFINITION  Human beta-2-adrenergic receptor mRNA, complete cds.
ACCESSION   M15169 J02728 M16106
VERSION     M15169.1  GI:178201
KEYWORDS    adrenergic receptor.
SOURCE      Homo sapiens (clone: pTF.) (tissue library: Evan Sadler) placenta
            cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Kobilka,B.K., Frielle,T., Dohlman,H.G., Bolanowski,M.A.,
            Dixon,R.A., Keller,P., Caron,M.G. and Lefkowitz,R.J.
  TITLE     Delineation of the intronless nature of the genes for the human and
            hamster beta 2-adrenergic receptor and their putative promoter
            regions
  JOURNAL   J. Biol. Chem. 262 (15), 7321-7327 (1987)
  MEDLINE   87222338
REFERENCE   2  (bases 1399 to 1985)
  AUTHORS   Kobilka,B.K., Dixon,R.A., Frielle,T., Dohlman,H.G.,
            Bolanowski,M.A., Sigal,I.S., Yang-Feng,T.L., Francke,U., Caron,M.G.
            and Lefkowitz,R.J.
  TITLE     cDNA for the human beta 2-adrenergic receptor: a protein with
            multiple membrane-spanning domains and encoded by a gene whose
            chromosomal location is shared with that of the receptor for
            platelet-derived growth factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (1), 46-50 (1987)
  MEDLINE   87092393
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="5q31-q32"
                     /clone="pTF."
                     /tissue_type="placenta"
                     /tissue_lib="Evan Sadler"
     mRNA            1369. .3383
                     /gene="ADRB2"
                     /note="b-2-adr mRNA (alt.); G00-120-541"
     gene            1369. .3383
                     /gene="ADRB2"
     mRNA            1376. .3383
                     /gene="ADRB2"
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  Query Match           100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity  100.0%;  Pred. No. 77;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCGG 1540
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                     /note="b-2-adr mRNA (alt.); G00-120-541"
     mRNA            1388. .3383
                     /gene="ADRB2"
                     /note="b-2-adr mRNA (alt.); G00-120-541"
     CDS             1487. .1546
                     /gene="ADRB2"
                     /note="putative"
                     /codon_start=1
                     /protein_id="AAA88014.1"
                     /db_xref="GI:560761"
                     /db_xref="GDB:G00-120-541"
                     /translation="MRLPGVRSRPAEPRRGSAR"
     CDS             1588. .2829
                     /gene="ADRB2"
                     /codon_start=1
                     /product="beta-2 adrenergic receptor"
                     /protein_id="AAA88015.1"
                     /db_xref="GI:178202"
                     /db_xref="GDB:G00-120-541"
                     /translation="MGQPGNGSAFLLAPNRSHAPDHDVTQQRDEVWVVGMGIVMSLIV
                     LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
                     NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                     IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                     AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                     TVPSDNIDSQGRNCSTNDSLL"
BASE COUNT      790 a    873 c    895 g    893 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 9
AC011354/c
LOCUS       AC011354              133042 bp    DNA     linear   PRI 27-JUN-2001
DEFINITION  Homo sapiens chromosome 5 clone CTC-354F19, complete sequence.
ACCESSION   AC011354
VERSION     AC011354.4  GI:14572125
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 133042)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 133042)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 133042)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jun 27, 2001 this sequence version replaced gi:13699555.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.9% of Sequence;
            Estimated Total Number of Errors is 0.1.
FEATURES             Location/Qualifiers
     source          1. .133042
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTC-354F19"
BASE COUNT    40170 a  26580 c  25753 g  40539 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 133042;
  Best Local Similarity   100.0%;  Pred. No. 45;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||||||||||||||||||
Db  127758 GGCTGGGGGCGCCTCAGCGG 127739


RESULT 10
AC011334/c
LOCUS       AC011334              134413 bp    DNA     linear   PRI 27-NOV-2001
DEFINITION  Homo sapiens chromosome 5 clone CTC-235N17, complete sequence.
ACCESSION   AC011334
VERSION     AC011334.5  GI:17105283
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 134413)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 134413)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 134413)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Nov 27, 2001 this sequence version replaced gi:12830127.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 100% of Sequence;
            Estimated Total Number of Errors is 0.
FEATURES             Location/Qualifiers
     source          1. .134413
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTC-235N17"
BASE COUNT    40269 a  28043 c  27434 g  38667 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 134413;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||||||||||||||||||
Db   54724 GGCTGGGGGCGCCTCAGCGG 54705


RESULT 11
AC027635
LOCUS       AC027635              142239 bp    DNA     linear   HTG 01-SEP-2000
DEFINITION  Homo sapiens chromosome 3 clone RP11-571C11, *** SEQUENCING IN
            PROGRESS ***, 60 unordered pieces.
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ACCESSION   AC027635
VERSION     AC027635.4  GI:9958288
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 142239)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 142239)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAR-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Sep 1, 2000 this sequence version replaced gi:7658491.

            ----------------- Genome Center -----------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            -------------- Project Information --------------
            Center project name: H_NH0571C11
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 100%
            Sequencing vector: plasmid; 0%
            Chemistry: Dye-primer ET; 100% of reads
            Chemistry: Dye-terminator Big Dye; 0% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 100609 bases at least Q40
            Consensus quality: 115224 bases at least Q30
            Consensus quality: 123413 bases at least Q20
            Insert size: 198000; agarose-fp
            Insert size: 135770; sum-of-contigs
            Quality coverage: 1.74 in Q20 bases; agarose-fp
            Quality coverage: 2.65 in Q20 bases; sum-of-contigs
            ------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 60 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1772: contig of 1772 bp in length
            *     1773     1872: gap of unknown length
            *     1873     3061: contig of 1189 bp in length
            *     3062     3161: gap of unknown length
            *     3162     4499: contig of 1338 bp in length
            *     4500     4599: gap of unknown length
            *     4600     5915: contig of 1316 bp in length
            *     5916     6015: gap of unknown length
            *     6016     7920: contig of 1905 bp in length
            *     7921     8020: gap of unknown length
            *     8021     9089: contig of 1069 bp in length
            *     9090     9189: gap of unknown length
            *     9190    10710: contig of 1521 bp in length
            *    10711    10810: gap of unknown length
            *    10811    11914: contig of 1104 bp in length
            *    11915    12014: gap of unknown length
            *    12015    13290: contig of 1276 bp in length
            *    13291    13390: gap of unknown length
            *    13391    15039: contig of 1649 bp in length
            *    15040    15139: gap of unknown length
            *    15140    16939: contig of 1800 bp in length
            *    16940    17039: gap of unknown length
            *    17040    18447: contig of 1408 bp in length
            *    18448    18547: gap of unknown length
            *    18548    19671: contig of 1124 bp in length
            *    19672    19771: gap of unknown length
            *    19772    22075: contig of 2304 bp in length
            *    22076    22175: gap of unknown length
            *    22176    24036: contig of 1861 bp in length
            *    24037    24136: gap of unknown length
            *    24137    25169: contig of 1033 bp in length
            *    25170    25269: gap of unknown length
            *    25270    26774: contig of 1505 bp in length
            *    26775    26874: gap of unknown length
            *    26875    28242: contig of 1368 bp in length
            *    28243    28342: gap of unknown length
            *    28343    31033: contig of 2691 bp in length
            *    31034    31133: gap of unknown length
            *    31134    32950: contig of 1817 bp in length
            *    32951    33050: gap of unknown length
            *    33051    34839: contig of 1789 bp in length
            *    34840    34939: gap of unknown length
            *    34940    36118: contig of 1179 bp in length
            *    36119    36218: gap of unknown length
            *    36219    37404: contig of 1186 bp in length
            *    37405    37504: gap of unknown length
            *    37505    38733: contig of 1229 bp in length
            *    38734    38833: gap of unknown length
            *    38834    40287: contig of 1454 bp in length
            *    40288    40387: gap of unknown length
            *    40388    42147: contig of 1760 bp in length
            *    42148    42247: gap of unknown length
            *    42248    44655: contig of 2408 bp in length
            *    44656    44755: gap of unknown length
            *    44756    46613: contig of 1858 bp in length
            *    46614    46713: gap of unknown length
            *    46714    48027: contig of 1314 bp in length
            *    48028    48127: gap of unknown length
            *    48128    50723: contig of 2596 bp in length
            *    50724    50823: gap of unknown length
            *    50824    53274: contig of 2451 bp in length
            *    53275    53374: gap of unknown length
            *    53375    55204: contig of 1830 bp in length
            *    55205    55304: gap of unknown length
            *    55305    57645: contig of 2341 bp in length
            *    57646    57745: gap of unknown length
            *    57746    59730: contig of 1985 bp in length
            *    59731    59830: gap of unknown length
            *    59831    62411: contig of 2581 bp in length
            *    62412    62511: gap of unknown length
            *    62512    64508: contig of 1997 bp in length
            *    64509    64608: gap of unknown length
            *    64609    67037: contig of 2429 bp in length
            *    67038    67137: gap of unknown length
            *    67138    70835: contig of 3698 bp in length
            *    70836    70935: gap of unknown length
            *    70936    74094: contig of 3159 bp in length
            *    74095    74194: gap of unknown length
            *    74195    77539: contig of 3345 bp in length
            *    77540    77639: gap of unknown length
            *    77640    80474: contig of 2835 bp in length
            *    80475    80574: gap of unknown length
            *    80575    83778: contig of 3204 bp in length
            *    83779    83878: gap of unknown length
            *    83879    86533: contig of 2655 bp in length
            *    86534    86633: gap of unknown length
            *    86634    89970: contig of 3337 bp in length
            *    89971    90070: gap of unknown length
            *    90071    93420: contig of 3350 bp in length
            *    93421    93520: gap of unknown length
            *    93521    95337: contig of 1817 bp in length
            *    95338    95437: gap of unknown length
            *    95438    97401: contig of 1964 bp in length
            *    97402    97501: gap of unknown length
            *    97502   101723: contig of 4222 bp in length
            *   101724   101823: gap of unknown length
            *   101824   104516: contig of 2693 bp in length
            *   104517   104616: gap of unknown length
            *   104617   107448: contig of 2832 bp in length
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            *   107449   107548: gap of unknown length
            *   107549   111408: contig of 3860 bp in length
            *   111409   111508: gap of unknown length
            *   111509   115340: contig of 3832 bp in length
            *   115341   115440: gap of unknown length
            *   115441   118918: contig of 3478 bp in length
            *   118919   119018: gap of unknown length
            *   119019   122741: contig of 3723 bp in length
            *   122742   122841: gap of unknown length
            *   122842   126444: contig of 3603 bp in length
            *   126445   126544: gap of unknown length
            *   126545   130312: contig of 3768 bp in length
            *   130313   130412: gap of unknown length
            *   130413   133649: contig of 3237 bp in length
            *   133650   133749: gap of unknown length
            *   133750   137465: contig of 3716 bp in length
            *   137466   137565: gap of unknown length
            *   137566   141165: contig of 3600 bp in length
            *   141166   141265: gap of unknown length
            *   141266   142239: contig of 974 bp in length.
FEATURES             Location/Qualifiers
     source          1. .142239
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /clone="RP11-571C11"
     misc_feature    1. .1772
                     /note="assembly_name:Contig62"
     misc_feature    1873. .3061
                     /note="assembly_name:Contig70"
     misc_feature    3162. .4499
                     /note="assembly_name:Contig78"
     misc_feature    4600. .5915
                     /note="assembly_name:Contig81"
     misc_feature    6016. .7920
                     /note="assembly_name:Contig84"
     misc_feature    8021. .9089
                     /note="assembly_name:Contig86"
     misc_feature    9190. .10710
                     /note="assembly_name:Contig89"
     misc_feature    10811. .11914
                     /note="assembly_name:Contig90"
     misc_feature    12015. .13290
                     /note="assembly_name:Contig93"
     misc_feature    13391. .15039
                     /note="assembly_name:Contig95"
     misc_feature    15140. .16939
                     /note="assembly_name:Contig96"
     misc_feature    17040. .18447
                     /note="assembly_name:Contig97"
     misc_feature    18548. .19671

  Query Match             95.0%;  Score 19;  DB 2;  Length 142239;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCG 19
          |||||||||||||||||||
Db 135440 GGCTGGGGGCGCCTCAGCG 135458


RESULT 12
BC012481/c
LOCUS       BC012481                2063 bp    mRNA    linear   PRI 20-AUG-2001
DEFINITION  Homo sapiens, Similar to adrenergic, beta-2-, receptor, surface,
            clone MGC:21367 IMAGE:4538187, mRNA, complete cds.
ACCESSION   BC012481
VERSION     BC012481.1  GI:15214693
KEYWORDS    MGC.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2063)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-AUG-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: villalon@bcm.tmc.edu.
            Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
            A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
            Muzny,D.M., Gibbs,R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 28 Row: k Column: 6
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 178203.
FEATURES             Location/Qualifiers
     source          1. .2063
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="MGC:21367 IMAGE:4538187"
                     /tissue_type="Prostate, adenocarcinoma."
                     /clone_lib="NIH_MGC_91"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             222. .1463
                     /codon_start=1
                     /product="Similar to adrenergic, beta-2-, receptor,
                     surface"
                     /protein_id="AAH12481.1"
                     /db_xref="GI:15214694"
                     /translation="MGQPGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
                     LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
                     NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                     IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                     AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                     TVPSDNIDSPGRNCSTNDSLL"
BASE COUNT      512 a    522 c    498 g    531 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 9;  Length 2063;
  Best Local Similarity   95.0%;  Pred. No. 4.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCGG 20
          |||||||||||||||||| |
Db    193 GGCTGGGGGCGCCTCAGCAG 174


RESULT 13
HSBAR/c
LOCUS       HSBAR                   2305 bp    DNA     linear   PRI 12-SEP-1993
DEFINITION  Human gene for beta-adrenergic receptor (beta-2 subtype).
ACCESSION   Y00106
VERSION     Y00106.1  GI:29370
KEYWORDS    beta-adrenergic receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 2305)
  AUTHORS   Schofield,P.R., Rhee,L.M. and Peralta,E.G.
  TITLE     Primary structure of the human beta-adrenergic receptor gene
  JOURNAL   Nucleic Acids Res. 15 (8), 3636 (1987)
  MEDLINE   87203400
REFERENCE   2  (bases 1 to 2305)
  AUTHORS   Schofield,P.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-OCT-1987)
FEATURES             Location/Qualifiers
     source          1. .2305
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="lambdahbetaAR17"
                     /clone_lib="Maniatis human"
     CDS             794. .2035
                     /note="beta-adrenergic receptor (AA 1 - 413)"
                     /codon_start=1
                     /protein_id="CAA68289.1"
                     /db_xref="GI:29371"
                     /db_xref="SWISS-PROT:P07550"
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                     /note="membrane spanning domain I"
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                     /note="membrane spanning domain II"
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                     /note="membrane spanning domain III"
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                     /note="membrane spanning domain IV"
     misc_feature    1385. .1450
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     misc_feature    1616. .1687
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     misc_feature    1712. .1774
                     /note="membrane spanning domain VII"
BASE COUNT      495 a    616 c    649 g    545 t
ORIGIN

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  Best Local Similarity   95.0%;  Pred. No. 4.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCGG 20
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Db    765 GGCTGGGGGCGCCTCAGCAG 746


RESULT 14
AX022517/c
LOCUS       AX022517               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9937761.
ACCESSION   AX022517
VERSION     AX022517.1  GI:10046115
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 1 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      794 a    871 c    892 g    894 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 3451;
  Best Local Similarity   95.0%;  Pred. No. 3.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCGG 20
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Db   1559 GGCTGGGGGCGCCTCAGCAG 1540


RESULT 15
AX022518/c
LOCUS       AX022518               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9937761.
ACCESSION   AX022518
VERSION     AX022518.1  GI:10046116
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 2 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
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BASE COUNT      790 a    872 c    895 g    894 t
ORIGIN

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  Best Local Similarity   95.0%;  Pred. No. 3.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCGG 20
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Db   1559 GGCTGGGGGCGCCTCAGCAG 1540


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Job time : 424.636 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 13:22:40 ; Search time 290.727 Seconds
(without alignments)
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Title: US-09-856-803-5
Perfect score: 15
Sequence: 1 gtccgcccgctgagg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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17: em_hum:*
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19: em_mu:*
20: em_om:*
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23: em_pat:*
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27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15	100.0	20	6	A65746	A65746 Sequence 27
2	15	100.0	51	6	AX204248	AX204248 Sequence
3	15	100.0	230	6	AR164456	AR164456 Sequence
4	15	100.0	1948	4	CFB2AR	X94608 C.familiari
5	15	100.0	1970	9	HSBARR	X04827 Human mRNA
6	15	100.0	2679	6	A65720	A65720 Sequence 1
7	15	100.0	3451	6	AX022519	AX022519 Sequence
8	15	100.0	3451	6	AX022522	AX022522 Sequence
9	15	100.0	3451	6	AX332732	AX332732 Sequence
10	15	100.0	3451	6	AX334116	AX334116 Sequence
11	15	100.0	3451	9	HUMADRBR	M15169 Human beta-
c 12	15	100.0	25883	1	AB008466	AB008466 Streptomy
c 13	15	100.0	42014	2	AC018327	AC018327 Drosophil
14	15	100.0	54705	2	AC103155	AC103155 Rattus no
15	15	100.0	133042	9	AC011354	AC011354 Homo sapi
16	15	100.0	134413	9	AC011334	AC011334 Homo sapi
c 17	15	100.0	160710	3	AC009537	AC009537 Drosophil
c 18	15	100.0	194030	2	AC095021	AC095021 Sus scrof
c 19	15	100.0	303209	3	AE003604	AE003604 Drosophil
c 20	14	93.3	744	9	HSA336392	AJ336392 Homo sapi
21	14	93.3	2360	1	AF006054	AF006054 Mycobacte
c 22	14	93.3	3087	3	AB034690	AB034690 Drosophil
c 23	14	93.3	4393	2	AC019406	AC019406 Drosophil
24	14	93.3	4393	3	AE003298	AE003298 Drosophil
25	14	93.3	4454	9	AB006756	AB006756 Homo sapi
26	14	93.3	4648	9	AB006755	AB006755 Homo sapi
27	14	93.3	4714	9	AB006757	AB006757 Homo sapi
c 28	14	93.3	5285	9	HUMVWFA31	M25858 Human von W
c 29	14	93.3	6153	6	AR065637	AR065637 Sequence
c 30	14	93.3	6153	6	AR096665	AR096665 Sequence
c 31	14	93.3	6360	6	AX334774	AX334774 Sequence
c 32	14	93.3	6360	9	HUMVWFM	M10321 Human von W
c 33	14	93.3	8575	9	HSVWFR1	X04385 Human mRNA
c 34	14	93.3	8588	6	I08449	I08449 Sequence 3
35	14	93.3	10570	1	AE005005	AE005005 Halobacte
36	14	93.3	12300	1	AE005887	AE005887 Caulobact
c 37	14	93.3	13076	1	AE002033	AE002033 Deinococc
38	14	93.3	13500	1	AE008064	AE008064 Agrobacte
39	14	93.3	14539	1	AE009099	AE009099 Agrobacte
40	14	93.3	15648	1	AE007021	AE007021 Mycobacte
c 41	14	93.3	19482	1	AE007072	AE007072 Mycobacte
42	14	93.3	27149	2	AC014204	AC014204 Drosophil
43	14	93.3	32806	1	MTV007	AL021184 Mycobacte
c 44	14	93.3	34150	1	MTCY190	Z70283 Mycobacteri
45	14	93.3	53736	2	AC068452	AC068452 Mus muscu

ALIGNMENTS

RESULT 1
A65746
LOCUS A65746 20 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 27 from Patent WO9735973.
ACCESSION A65746
VERSION A65746.1 GI:4531364
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lenzen,G., Pietri-Rouxel,F., Drumare, Marie-Francoise and Strosberg,A.D.
TITLE CANINE beta 2- AND beta 3-ADRENERGIC RECEPTORS AND USE THEREOF
JOURNAL Patent: WO 9735973-A 27 02-OCT-1997;
VETIGEN (FR)
COMMENT Other publication FR 2746813 19971003.
FEATURES Location/Qualifiers
source 1. .20
/organism="unidentified"
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BASE COUNT 2 a 8 c 8 g 2 t
ORIGIN

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Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db      6 GTCCGCCCGCTGAGG 20


RESULT 2
AX204248
LOCUS       AX204248                 51 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 354 from Patent WO0148245.
ACCESSION   AX204248
VERSION     AX204248.1  GI:15393760
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0148245-A 354 05-JUL-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     variation       26
                     /note="single nucleotide polymorphism
                     Accession number cg43040273"
BASE COUNT        5 a      24 c      18 g       4 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 9.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
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Db     19 GTCCGCCCGCTGAGG 33


RESULT 3
AR164456
LOCUS       AR164456                 230 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 8 from patent US 6273893.
ACCESSION   AR164456
VERSION     AR164456.1  GI:16237489
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 230)
  AUTHORS   McAllen,J. III, Overaker,D.W. and Cooper,K.L.
  TITLE     Absorbable rivet/pin applier for use in surgical procedures
  JOURNAL   Patent: US 6273893-A 8 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .230
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BASE COUNT       42 a      91 c      70 g      27 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
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Db    166 GTCCGCCCGCTGAGG 180


RESULT 4
CFB2AR
LOCUS       CFB2AR                   1948 bp    mRNA    linear   MAM 27-JAN-1997
DEFINITION  C.familiaris mRNA for beta2-adrenergic receptor.
ACCESSION   X94608
VERSION     X94608.1  GI:1359588
KEYWORDS    beta-2 adrenergic receptor.
SOURCE      dog.
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 1948)
  AUTHORS   Emala,C.W., Kuhl,J., Hirshman,C.A. and Levine,M.A.
  TITLE     Rapid communication: cloning and sequencing of a canine beta
            2-adrenergic receptor cDNA
  JOURNAL   J. Anim. Sci. 74 (9), 2285 (1996)
  MEDLINE   97034778
REFERENCE   2  (bases 1 to 1948)
  AUTHORS   Emala,C.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-DEC-1995) C.W. Emala, Johns Hopkins School of
            Medicine, Dept of Anesthesiology, John Hopkins Hospital, Meyer
            297A, Baltimore Maryland 21287, USA
FEATURES             Location/Qualifiers
     source          1. .1948
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                     /db_xref="taxon:9615"
                     /tissue_type="cardiac muscle"
     CDS             151. .1398
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                     IIMGTFTLCWLPFFIVNIVHVIQDNLIPKEVYILLNWVGYVNSAFNPLIYCRSPDFRI
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                     QGTVPSDSVDSQGRNCSTNDSLL"
BASE COUNT      395 a     539 c     540 g     474 t
ORIGIN

  Query Match            100.0%;  Score 15;  DB 4;  Length 1948;
  Best Local Similarity  100.0%;  Pred. No. 7.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db    104 GTCCGCCCGCTGAGG 118


RESULT 5
HSBARR
LOCUS       HSBARR                   1970 bp    mRNA    linear   PRI 12-SEP-1993
DEFINITION  Human mRNA for brain beta-adrenergic receptor.
ACCESSION   X04827
VERSION     X04827.1  GI:29372
KEYWORDS    beta-adrenergic receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1970)
  AUTHORS   Chung,F.Z., Lentes,K.U., Gocayne,J., Fitzgerald,M., Robinson,D.,
            Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
  TITLE     Cloning and sequence analysis of the human brain beta-adrenergic
            receptor. Evolutionary relationship to rodent and avian
            beta-receptors and porcine muscarinic receptors
```

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  JOURNAL   FEBS Lett. 211 (2), 200-206 (1987)
  MEDLINE   87105974
REFERENCE   2  (bases 1 to 1970)
  AUTHORS   Kerlavage,A.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-SEP-1987)
COMMENT     substantial corrections are reported in [2]
            Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
FEATURES             Location/Qualifiers
     source          1. .1970
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                     /db_xref="taxon:9606"
                     /clone_lib="neonatal human brain stem"
     CDS             178. .1419
                     /note="beta-adrenergic receptor (AA 1-413)"
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     misc_feature    1491. .1496
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 7.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
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Db     124 GTCCGCCCGCTGAGG 138


RESULT 6
A65720
LOCUS       A65720                  2679 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 1 from Patent WO9735973.
ACCESSION   A65720
VERSION     A65720.1  GI:4531340
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2679)
  AUTHORS   Lenzen,G., Pietri-Rouxel,F., Drumare, Marie-Francoise and
            Strosberg,A.D.
  TITLE     CANINE beta 2- AND beta 3-ADRENERGIC RECEPTORS AND USE THEREOF
  JOURNAL   Patent: WO 9735973-A 1 02-OCT-1997;
            VETIGEN (FR)
COMMENT     Other publication FR 2746813 19971003.
FEATURES             Location/Qualifiers
     source          1. .2679
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                     /db_xref="taxon:32644"
BASE COUNT      577 a    736 c    724 g    642 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 7.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db     122 GTCCGCCCGCTGAGG 136


RESULT 7
AX022519
LOCUS       AX022519                3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 3 from Patent WO9937761.
ACCESSION   AX022519
VERSION     AX022519.1  GI:10046118
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 3 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
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BASE COUNT      789 a    872 c    897 g    893 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 7.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db    1534 GTCCGCCCGCTGAGG 1548


RESULT 8
AX022522
LOCUS       AX022522                3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 6 from Patent WO9937761.
ACCESSION   AX022522
VERSION     AX022522.1  GI:10046121
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 6 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      789 a    873 c    897 g    892 t
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 7.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 GTCCGCCCGCTGAGG 15
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Db   1534 GTCCGCCCGCTGAGG 1548


RESULT 9
AX332732
LOCUS       AX332732               3451 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 3241 from Patent WO0194629.
ACCESSION   AX332732
VERSION     AX332732.1  GI:18123366
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 3241 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .3451
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                     /db_xref="taxon:9606"
BASE COUNT      790 a    873 c    895 g    893 t
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 7.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db   1534 GTCCGCCCGCTGAGG 1548


RESULT 10
AX334116
LOCUS       AX334116               3451 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 4625 from Patent WO0194629.
ACCESSION   AX334116
VERSION     AX334116.1  GI:18124835
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 4625 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      790 a    873 c    895 g    893 t
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 7.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCCGCTGAGG 15
          |||||||||||||||
Db   1534 GTCCGCCCGCTGAGG 1548


RESULT 11
HUMADRBR
LOCUS       HUMADRBR               3451 bp    mRNA    linear   PRI 13-FEB-1996
DEFINITION  Human beta-2-adrenergic receptor mRNA, complete cds.
ACCESSION   M15169 J02728 M16106
VERSION     M15169.1  GI:178201
KEYWORDS    adrenergic receptor.
SOURCE      Homo sapiens (clone: pTF.) (tissue library: Evan Sadler) placenta
            cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Kobilka,B.K., Frielle,T., Dohlman,H.G., Bolanowski,M.A.,
            Dixon,R.A., Keller,P., Caron,M.G. and Lefkowitz,R.J.
  TITLE     Deli.eation of the intronless nature of the genes for the human and
            hamster beta 2-adrenergic receptor and their putative promoter
            regions
  JOURNAL   J. Biol. Chem. 262 (15), 7321-7327 (1987)
  MEDLINE   87222338
REFERENCE   2  (bases 1399 to 1985)
  AUTHORS   Kobilka,B.K., Dixon,R.A., Frielle,T., Dohlman,H.G.,
            Bolanowski,M.A., Sigal,I.S., Yang-Feng,T.L., Francke,U., Caron,M.G.
            and Lefkowitz,R.J.
  TITLE     cDNA for the human beta 2-adrenergic receptor: a protein with
            multiple membrane-spanning domains and encoded by a gene whose
            chromosomal location is shared with that of the receptor for
            platelet-derived growth factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (1), 46-50 (1987)
  MEDLINE   87092393
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="5q31-q32"
                     /clone="pTF."
                     /tissue_type="placenta"
                     /tissue_lib="Evan Sadler"
     mRNA            1369. .3383
                     /gene="ADRB2"
                     /note="b-2-adr mRNA (alt.); G00-120-541"
     gene            1369. .3383
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     mRNA            1376. .3383
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                     /note="b-2-adr mRNA (alt.); G00-120-541"
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                     /note="b-2-adr mRNA (alt.); G00-120-541"
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                     /gene="ADRB2"
                     /note="b-2-adr mRNA (alt.); G00-120-541"
     CDS             1487. .1546
                     /gene="ADRB2"
                     /note="putative"
                     /codon_start=1
                     /protein_id="AAA88014.1"
                     /db_xref="GI:560761"
                     /db_xref="GDB:G00-120-541"
                     /translation="MRLPGVRSRPAEPRRGSAR"
     CDS             1588. .2829
                     /gene="ADRB2"
                     /codon_start=1
                     /product="beta-2 adrenergic receptor"
                     /protein_id="AAA88015.1"
                     /db_xref="GI:178202"
                     /db_xref="GDB:G00-120-541"
                     /translation="MGQPGNGSAFLLAPNRSHAPDHDVTQQRDEVWVVGMGIVMSLIV
                     LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
                     NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
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                     IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                     AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                     TVPSDNIDSQGRNCSTNDSLL"
BASE COUNT      790 a    873 c    895 g    893 t
ORIGIN

  Query Match           100.0%;  Score 15;  DB 9;  Length 3451;
  Best Local Similarity  100.0%;  Pred. No. 7.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCCGCTGAGG 15
           |||||||||||||||
Db    1534 GTCCGCCCGCTGAGG 1548


RESULT 12
AB008466/c
LOCUS       AB008466               25883 bp    DNA     linear   BCT 16-NOV-2001
DEFINITION  Streptomyces galilaeus aklavinone-aclacinomycin biosynthesis gene
            cluster, complete cds.
ACCESSION   AB008466
VERSION     AB008466.1  GI:16945704
KEYWORDS    .
SOURCE      Streptomyces galilaeus (strain:3AR-33) DNA.
  ORGANISM  Streptomyces galilaeus
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE   1  (bases 1 to 25883)
  AUTHORS   Fujii,I. and Chung,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-OCT-1997) Isao Fujii, The University of Tokyo,
            Gragduate School of Pharmaceutical Sciences; 7-3-1 Hongo,
            Bunkyo-ku, Tokyo 113-0033, Japan
            (E-mail:ifujii@mol.f.u-tokyo.ac.jp, Tel:81-3-5841-4743,
            Fax:81-3-5841-4744)
FEATURES             Location/Qualifiers
     source          1. .25883
                     /organism="Streptomyces galilaeus"
                     /strain="3AR-33"
                     /db_xref="taxon:33899"
     gene            complement(164. .1039)
                     /gene="aclY"
     CDS             complement(164. .1039)
                     /gene="aclY"
                     /function="dTDP-1-glucose synthase"
                     /note="putative"
                     /codon_start=1
                     /transl_table=11
                     /product="AclY"
                     /protein_id="BAB72036.1"
                     /db_xref="GI:16945705"
                     /translation="MKGIILAGGSGTRLHPITVSVSKQLLPVGDKPMIYYPLSVLMLA
                     DIREILLICTERDLEQFRRLLGDGSQLGLRIDYAVQNRPAGLADAFVIGADHVGDDDV
                     ALVLGDNIFHGHHFYDLLQSNVRDVQGCVLFGYPVEDPERYGVGETDASGQLVSLEEK
                     PLRPRSDLAITGLYLYDNEVVDIAKNLRPSARGELEITDVNRNYLARGRARLVDLGRG
                     FAWLDAGTPESLLQATQYVRTLEERQGVRIACVEEVAVRMGFIDADMCHRLGEQMSQS
                     GYGRYVMAVAREFSG"
     gene            1274. .2383
                     /gene="aclZ"
     CDS             1274. .2383
                     /gene="aclZ"
                     /function="aminotransferase"
                     /note="putative"
                     /codon_start=1
                     /transl_table=11
                     /product="AclZ"
                     /protein_id="BAB72037.1"
                     /db_xref="GI:16945706"
                     /translation="MTTLVWDYLQEYENERADILDAVETVFSSGRLVLGDSVRGFEEE
                     FAAYHGAAHCVGVDNGTNAIKLALQALGVGPGDEVVTVSNTAAPTIVAIDSVGATPVF
                     VDIHADSYLMDTEQVEAAITPRTRCLLPVHLYGQCVDLAPLERLAAEHDLFLVEDCAQ
                     AHGARRAGRLAGTTGDAAAFSFYPTKVLGAYGDGGAVLTSRDDAHHALRRLRYYGMEE
                     RYYVVGTPGHNARLDEVQAEILQRKLRRLDTYIEGRRAVARSYEDGLGDTALVLPHTV
                     PGNENVYYVYTVRHPRRDDIIKALKAYDIELNISYPWPVHTMSGFAHLGYGKGSLPVT
                     EDLAGQIFSLPMYPALPPDAQDKVISAVRDVLDSL"
gene            complement(2466. .3818)
                /gene="aclN"
CDS             complement(2466. .3818)
                /gene="aclN"
                /function="dTDP-hexose 2,3-dehydratase"
                /note="putative"
                /codon_start=1
                /transl_table=11
                /product="AclN"
                /protein_id="BAB72038.1"
                /db_xref="GI:16945707"
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                LAALDQWYETPVTGDLRHRTGKFFTVHGLRVHDPTGAVHWWDQPIIDQPEVGILGILV
                KEFDGVPHFLMQAKAEPGNPGGLQLSPTVQATRSNYTGVHKGRPVPYLDYFRDTSRHR
                VIADVRQSEQGAWFYRKRNRNMVVETTTEVEVLEGFRWFTLGQLYLLLSRDDIVNMDA
                RTVMACLPARSRPDGALHRTTDVLSWITGARSLAGVSTQRIALSGLDEWEHTDMGYSH
                ESGGFFDVIGVSVTANGREVGGWRQAMIEPHGTGVIAFLMRRINGVEHVLVHARTEPG
                YADVVELAPTVQCVPESYRWLPSAARPRHLDEVLAAGPDRIRFEAVLSEEGGRFFHAR
                NRYLIVDSDVPEDPGHPDYRWLSMDQLTGLLRHSHYLNVQARSLVACLRGLETARSAR
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gene            complement(3963. .4856)
                /gene="aclM"
CDS             complement(3963. .4856)
                /gene="aclM"
                /function="dTDP-4-keto-6-deoxyhexose reductase"
                /note="putative"
                /codon_start=1
                /transl_except=(pos:complement(4854. .4856),aa:Met)
                /transl_table=11
                /product="AclM"
                /protein_id="BAB72039.1"
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                AVPPAELARLLTGHRVRAVVNVTGGWGTTEEEMRYAHITLVDRLLRALALMDDRPRLV
                HVGSVHEYGPVPEPLSIGEDLPPRPTTMYARTKLAGSELVLDAARAGRVDALVLRAVN
                VCGPRTTRASFLGRSPACCGPPTRRTRVTLRLADARRDFVDVRDLAEAVVLALAAPAT
                GRVVNIGRGEATSMRELVDLLAAAAALPPDALRIEDGPIDSKGGNWTLADIGLAGRLL
                GWKRRIPLAEAMRATWEVPAD"
gene            complement(4895. .5500)
                /gene="aclL"
CDS             complement(4895. .5500)
                /gene="aclL"
                /function="dTDP-4-keto-6-deoxyhexose 3,5-epimerase"
                /note="putative"
                /codon_start=1
                /transl_except=(pos:complement(5498. .5500),aa:Met)
                /transl_table=11
                /product="AclL"
                /protein_id="BAB72040.1"
                /db_xref="GI:16945709"
                /translation="MQFRELAVSGAFVFTPPVFEDDRDLFTSPFQEPAFVAALGHPLF
                PVAQSNHSRSRRGTVRGIHYTVTPPGVAKYVYCARGRAIDIVVDIRVGSPTYGRWDSS
                VLDPEGFRAMYFPVGVGHAFIALEDDTVMSYMLSGSYEAQHEMSLSPLDPALGLPIPQ
                DVAPLLSARDTAAPLLEQVRAEGGLPEYDKCRRIEAALWRP"
gene            complement(5513. .6835)
                /gene="aclK"
CDS             complement(5513. .6835)
                /gene="aclK"
                /function="glycosyltransferase"
                /note="putative"
                /codon_start=1
                /transl_table=11
                /product="AclK"
                /protein_id="BAB72041.1"
                /db_xref="GI:16945710"
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                FGLDLLGRMRETFLDLQEERLPEQRDDPLREWLTWTLGRYGAEFEEEVAVGQWTVDPV
                PPSMRFPVKQPFVPLRYIPYNGQAVIPDWLHEPPKKRRVCLTLGVAHREVLDGDRASI
                GELVKALAELDVEVVATLNGEAARRDGLPDNVRAVDFVPLNALLPTCSAVIHHGGSGT
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                FQTALAHGVPQLIVPDMVWDTIHKAKQLERFGAGLYLHDVDNYTAQDLRDHLLRLLEE
gene            PSFAENCARIRREMVGTPSPNDIVPLLEKLTAEHRRDRGARGTVEGEQ"
CDS             complement(6921. .8273)
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                complement(6921. .8273)
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                /note="putative"
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                /transl_table=11
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                /protein_id="BAB72042.1"
                /db_xref="GI:16945711"
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                ERSGEEERLRIWATANGEVKSWTSRRTLDRAGLRIRFRQEVSQDPVAAMGGEWIVEAL
                PGGASRVRLLHDFRAVDDLERNVSWILEAIERNSGAELAALESAALRTGTDEAPYTFE
                DSVRIDAPAQDVRDFLHDAGQWQERLPHVARVLLKEDTPDVQHLEMDTRTPDGSTHTT
                ASVRICLPDGRIAYKQLQTPALMSVHTGEWSVREIPSGCVAVSRHTVVVNAAAVTKVL
                GASATTADARTFIRDALGGNSTITMRHAKEYAEERAGTEPVAPAEYASVQRFYAGQMR
                LLDEGEGDAWADTFTEDGTFDQSSFAEPVRGRAAIAAAVRGRPAAPAGTVRRHWLGLP
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gene            "
CDS             complement(8321. .9106)
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                complement(8321. .9106)
                /gene="aknA"
                /function="ketoreductase"
                /note="Registered with the DDBJ/EMBL/GenBank databases by
                the name of aknIII gene (12-JAN-1993). The accession
                number is D14040.
                putative"
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                /transl_table=11
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                HTVKELREAGHDVDGASCDVRDTARVRAFVQEARDRFGPVDVLVNNAGRSGGGHTAQI
                PDELWLDVIETNLNSVFRMTREVLTTGGMLERGAGRIVNIASTGGKQGVALGAPYSAS
                KHGVVGFTKALGLELAKTGITVNAVCPGYVETPMAERVRQGYAGAWDITEDEVLERFE
gene            AKIPLGRYSTPDEVAGLVGYLLSSTAASITAQAMNVCGGLGNY"
CDS             9319. .9687
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                9319. .9687
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                /codon_start=1
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                /db_xref="GI:16945713"
                /translation="MTDHEPGTEGADAVTFVNTFTVHAEPEVFEKEFARTSEFMARQP
                GFVRHTLCRHAERPGQYVNVAEWRDLASFRAAVSHDDFRPHAGALRALSESRPELYLV
gene            RLRREGAPGLDGPASEGEEI"
CDS             9684. .10955
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                EFRSRMAAECDFDGVRSGLTVRDTARLDRATQFAVVAAREALADSGIEIDERNAHRTG
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                GPAALVSAGCTSGLDSLGHALDLIREGAVDIMIAGGSDAPIAPITVACFDAIKATSPR
                NDTPEHASRPFDRTRSGFVLGEGAAVLVLEERESALRRGAQIYAEIAGYAGRANAHHM
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Mon No

100.0%; Score 15; DB 1; Length 25883;

Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GTCCGCCCCGCTGAGG 15
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Db   2478 GTCCGCCCCGCTGAGG 2464
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RESULT 13
AC018327/c
LOCUS AC018327
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pieces. 42014 bp DNA linear HTG 09-DEC-1999
ACCESSION AC018327
VERSION AC018327.1 GI:6552864
KEYWORDS HTG; HTGS_PHASE2.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 42014)
AUTHORS Adams,M. and Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
COMMENT This sequence was identified as CDM:10214360 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES Location/Qualifiers
source 1. .42014
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
BASE COUNT 12567 a 8420 c 8766 g 12261 t
ORIGIN

Query Match 100.0%; Score 15; DB 2; Length 42014;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GTCCGCCCGCTGAGG 15
          ||||||||||||||||
Db   2545 GTCCGCCCGCTGAGG 2531
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RESULT 14
AC103155
LOCUS AC103155
DEFINITION Rattus norvegicus clone CH230-201I4, *** SEQUENCING IN PROGRESS ***, 32 unordered pieces. 54705 bp DNA linear HTG 21-DEC-2001
ACCESSION AC103155
VERSION AC103155.2 GI:17974642
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 54705)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.,
Dugan-Rocha,S., Durbin,

Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louiseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 54705)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Dec 21, 2001 this sequence version replaced gi:17062799.
---------- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
---------- Project Information
Center project name: GJIW
Center clone name: CH230-201I4
---------- Summary Statistics
Assembly program: Phrap; version 0.990329First call to findPhrapList
Consensus quality: 42106 bases at least Q40
Consensus quality: 46901 bases at least Q30
Consensus quality: 50808 bases at least Q20
Estimated insert size: 23322; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.2x in Q20 bases; sum-of-contigs estimation
----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

*	1	3316: contig of 3316 bp in length
*	3317	3416: gap of unknown length
*	3417	7397: contig of 3981 bp in length
*	7398	7497: gap of unknown length
*	7498	10006: contig of 2509 bp in length
*	10007	10106: gap of unknown length
*	10107	12568: contig of 2462 bp in length
*	12569	12668: gap of unknown length
*	12669	14319: contig of 1651 bp in length
*	14320	14419: gap of unknown length
*	14420	15488: contig of 1069 bp in length
*	15489	15588: gap of unknown length
*	15589	17688: contig of 2100 bp in length
*	17689	17788: gap of unknown length
*	17789	19433: contig of 1645 bp in length
*	19434	19533: gap of unknown length
*	19534	20867: contig of 1334 bp in length
*	20868	20967: gap of unknown length
*	20968	22905: contig of 1938 bp in length
*	22906	23005: gap of unknown length
*	23006	24587: contig of 1582 bp in length
*	24588	24687: gap of unknown length
*	24688	26166: contig of 1479 bp in length
*	26167	26266: gap of unknown length
*	26267	27652: contig of 1386 bp in length
*	27653	27752: gap of unknown length
*	27753	29291: contig of 1539 bp in length
*	29292	29391: gap of unknown length
*	29392	30473: contig of 1082 bp in length
*	30474	30573: gap of unknown length
*	30574	31786: contig of 1213 bp in length
*	31787	31886: gap of unknown length
*	31887	33251: contig of 1365 bp in length
*	33252	33351: gap of unknown length
*	33352	34923: contig of 1572 bp in length
*	34924	35023: gap of unknown length
*	35024	37147: contig of 2124 bp in length
*	37148	37247: gap of unknown length
*	37248	38414: contig of 1167 bp in length
*	38415	38514: gap of unknown length
*	38515	40163: contig of 1649 bp in length
*	40164	40263: gap of unknown length
*	40264	41310: contig of 1047 bp in length
*	41311	41410: gap of unknown length
*	41411	42520: contig of 1110 bp in length
*	42521	42620: gap of unknown length
*	42621	44053: contig of 1433 bp in length
*	44054	44153: gap of unknown length
*	44154	45174: contig of 1021 bp in length
*	45175	45274: gap of unknown length
*	45275	46828: contig of 1554 bp in length
*	46829	46928: gap of unknown length
*	46929	47963: contig of 1035 bp in length
*	47964	48063: gap of unknown length
*	48064	49625: contig of 1562 bp in length
*	49626	49725: gap of unknown length
*	49726	50929: contig of 1204 bp in length
*	50930	51029: gap of unknown length
*	51030	52441: contig of 1412 bp in length
*	52442	52541: gap of unknown length
*	52542	53567: contig of 1026 bp in length
*	53568	53667: gap of unknown length
*	53668	54705: contig of 1038 bp in length.

FEATURES Location/Qualifiers
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/db_xref="taxon:10116"
/clone="CH230-201I4"

BASE COUNT 12220 a 14356 c 12411 g 12437 t 3281 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGCCCGCTGAGG 15
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Db 54238 GTCCGCCCGCTGAGG 54252

RESULT 15

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;
     AC011354              133042 bp    DNA     linear   PRI 27-JUN-2001
ION  Homo sapiens chromosome 5 clone CTC-354F19, complete sequence.
)N   AC011354
     AC011354.4  GI:14572125
;    HTG.
     human.
ISM  Homo sapiens
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
:E   1  (bases 1 to 133042)
<S   DOE Joint Genome Institute and Stanford Human Genome Center.
     Direct Submission
AL   Unpublished
:E   2  (bases 1 to 133042)
RS   DOE Joint Genome Institute.
     Direct Submission
AL   Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
     Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
:E   3  (bases 1 to 133042)
RS   DOE Joint Genome Institute and Stanford Human Genome Center.
     Direct Submission
AL   Submitted (27-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
     Drive, Walnut Creek, CA 94598, USA
     On Jun 27, 2001 this sequence version replaced gi:13699555.
     Draft Sequence Produced by DOE Joint Genome Institute
     www.jgi.doe.gov
     Finishing Completed at Stanford Human Genome Center
     www-shgc.stanford.edu
     Quality: Phrap Quality >=40 99.9% of Sequence;
     Estimated Total Number of Errors is 0.1.
S              Location/Qualifiers
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               /db_xref="taxon:9606"
               /chromosome="5"
               /clone="CTC-354F19"
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Local Similarity   100.0%;  Pred. No. 6.1e+02;
:s   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

 1 GTCCGCCCGCTGAGG 15
   |||||||||||||||
33 GTCCGCCCGCTGAGG 127747


completed: November  2, 2002, 16:49:20
e : 316.727 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 13:09:44 ; Search time 82.7273 Seconds
(without alignments)
415.078 Million cell updates/sec

Title: US-09-856-803-9
Perfect score: 20
Sequence: 1 ggctgggggcgcctcagcgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
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7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	21	AAA46129	Human beta2 adrene
c	2	20	100.0	51	22	AAH79739	Human DNA containi
c	3	20	100.0	230	22	AAH27139	Human beta-2 adren
c	4	20	100.0	1999	18	AAT93250	Beta-2 adrenalin r
c	5	20	100.0	2340	21	AAA38784	Human beta2 adrene
c	6	20	100.0	3451	19	AAV52614	Human beta-2-adren
c	7	20	100.0	3451	20	AAZ00776	Human beta 2-adren
c	8	20	100.0	3451	20	AAZ00779	Human beta 2-adren
c	9	20	100.0	3451	20	AAZ00773	Human beta 2-adren
c	10	20	100.0	3451	21	AAA38339	Human beta-adrener
c	11	20	100.0	3451	24	AAS18444	Reference sequence
	12	18.4	92.0	20	21	AAA46130	Human beta2 adrene
c	13	18.4	92.0	2300	20	AAX61116	Human beta2-adrene
c	14	18.4	92.0	2305	21	AAA38340	Human beta-adrener
c	15	18.4	92.0	3451	20	AAZ00774	Human beta 2-adren
c	16	18.4	92.0	3451	20	AAZ00775	Human beta 2-adren
c	17	18.4	92.0	3451	20	AAZ00777	Human beta 2-adren
c	18	18.4	92.0	3451	20	AAZ00778	Human beta 2-adren
c	19	18.4	92.0	3451	20	AAZ00780	Human beta 2-adren
	20	17	85.0	472	22	ABA43331	Human breast cell
	21	17	85.0	472	22	ABA53772	Human foetal liver
	22	17	85.0	472	22	ABA23521	Probe #1987 for ge
	23	17	85.0	472	22	AAK02034	Human brain expres
	24	17	85.0	472	22	AAK27490	Human bone marrow
	25	17	85.0	472	22	AAI12067	Probe #2000 for ge
	26	17	85.0	472	22	AAI33402	Probe #2088 used t
	27	17	85.0	472	22	AAI01990	Probe #1981 used t
	28	16.8	84.0	735	21	AAC98842	Human pancreatic c
	29	16.8	84.0	901	20	AAZ41406	Human normal pancr
	30	16.8	84.0	1149	21	AAA61733	cDNA encoding huma
c	31	16.8	84.0	2934	19	AAV41922	Nucleotide sequenc
c	32	16.8	84.0	3323	21	AAC98205	Human colon cancer
	33	16.8	84.0	3381	22	AAL02709	Human reproductive
c	34	16.8	84.0	3679	22	AAK52656	Human polynucleoti
c	35	16.8	84.0	3725	22	AAH78245	Nucleotide sequenc
c	36	16.8	84.0	3760	22	AAK51672	Human polynucleoti
c	37	16.8	84.0	29411	22	AAK76613	*Human immune/haema*
c	38	15.8	79.0	544	19	AAV69687	Human glial cell l
c	39	15.8	79.0	776	20	AAX28053	Human GDNF promote
	40	15.8	79.0	963	22	AAC89281	Human brain T calc
c	41	15.8	79.0	1207	19	AAV69688	Glial cell line-de
	42	15.8	79.0	1209	23	ABL27435	Drosophila melanog
	43	15.8	79.0	1228	22	AAH26058	Human PPT-I gene p
	44	15.8	79.0	1286	22	AAH26057	Human PPT-I gene p
c	45	15.8	79.0	1927	22	AAH76376	Murine adipocytes-

ALIGNMENTS

RESULT 1
AAA46129
ID AAA46129 standard; DNA; 20 BP.
XX
AC AAA46129;
XX
DT 05-OCT-2000 (first entry)
XX
DE Human beta2 adrenergic receptor beta2AR C allele-specific primer #2.
XX
KW Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW congestive heart failure; ischemic heart disease; arrhythmia;
KW obesity; diabetes; vascular disease; premature labour; migraine;
KW anaphylaxis; chronic obstructive pulmonary disease;
KW allele-specific oligonucleotide primer; ss.
XX
OS Homo sapiens.
XX
PN WO200031307-A1.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US27963.
XX
PR 25-NOV-1998; 98US-0109886.
XX
PA (UYCI-) UNIV CINCINNATI.
XX
PI Liggett SB;
XX
DR WPI; 2000-400107/34.

XX
PT Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT receptor (beta 2 AR), useful for predicting genetic disposition to a
PT disease modified by beta 2 AR expression e.g. congestive heart failure,
PT hypertension -
XX
PS Claim 8; Page 12; 56pp; English.
XX
CC The present sequence is an allele-specific oligonucleotide primer
CC for the C allele of the human beta2 adrenergic receptor (beta2AR) gene,
CC which is located on chromosome 5q31 (12). The gene has two different
CC alleles, and it has been shown that the presence of two copies of the T
CC allele leads to higher expression of the gene. This is because the
CC polymorphism is found in the 5' leader sequence, which encodes a peptide
CC which regulates expression of the beta2AR gene. The polymorphism is
CC thought to affect individuals' responses to beta-agonists and
CC beta-antagonists, and is likely to influence their predisposition to
CC asthma, hypertension, congestive heart failure, ischemic heart disease,
CC arrhythmia, obesity, diabetes, vascular disease, premature labour,
CC migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD).
CC The gene can, therefore, be used to predict the susceptibility of an
CC individual to these diseases and determine the best treatment.
XX
SQ Sequence 20 BP; 1 A; 6 C; 11 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGGGCGCCTCAGCGG 20
||||||||||||||||||||
Db 1 GGCTGGGGGCGCCTCAGCGG 20

RESULT 2
AAH79739/c
ID AAH79739 standard; DNA; 51 BP.
XX
AC AAH79739;
XX
DT 19-SEP-2001 (first entry)
XX
DE Human DNA containing single nucleotide polymorphism SEQ ID NO. 354.
XX
KW Human; single nucleotide polymorphism; SNP; angiopoietin;
KW 4-hydroxybutyrate; dehydrogenase; protein therapy;
KW adenosine triphosphate-dependent RNA helicase;
KW major histocompatibility complex Class I histocompatibility antigen; MHC;
KW phosphoglycerate kinase; immunosuppressive; immunostimulatory;
KW antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
KW antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200148245-A2.
XX
PD 05-JUL-2001.
XX
PF 27-DEC-2000; 2000WO-US35346.
XX
PR 27-DEC-1999; 99US-0472688.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-418297/44.
XX
PT Polymorphic nucleic acids encoding e.g. angiopoietin, dehydrogenase,
PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
PT diseases and infections -
XX
PS Claim 1; Page 162; 484pp; English.
XX
CC The invention relates to nucleic acids (AAH79386-AAH80036) encoding
CC polymorphic variants of proteins (AAG98010-AAG98238) related to
CC angiopoietin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
CC proteins have potential immunosuppressive, immunostimulatory,
CC antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
CC antileukemic, neuroprotective and antimicrobial activity and may be
CC useful in gene/protein therapy, vaccines, modulation of the expression
CC and activity of proteins related to angiopoietin, 4-hydroxybutyrate,
CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase,
CC major histocompatibility complex (MHC) Class I histocompatibility antigen
CC and/or phosphoglycerate kinase. Disorders that may be prevented,
CC diagnosed and/or treated by the above methods include multifactorial
CC diseases with a genetic component, such as autoimmune diseases (e.g.
CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
CC erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers
CC of the bladder, brain, breast, colon and kidney, leukemia), diseases of
CC the nervous system, an infection of pathogenic organisms. They may also
CC be used to alter phenotypic traits such as longevity, appearance,
CC strength, speed and endurance.
XX
SQ Sequence 51 BP; 5 A; 24 C; 18 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGGGCGCCTCAGCGG 20
||||||||||||||||||||
Db 44 GGCTGGGGGCGCCTCAGCGG 25

RESULT 3
AAH27139/c
ID AAH27139 standard; DNA; 230 BP.
XX
AC AAH27139;
XX
DT 08-AUG-2001 (first entry)
XX
DE Human beta-2 adrenergic receptor UTR region with RBP binding ability.
XX
KW Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration;
KW stroke; cardiovascular disease; hypertension; cancer; inflammation;
KW metabolic disorder; obesity; diabetes; beta-2 adrenergic receptor; ds.
XX
OS Homo sapiens.
XX
PN WO200134624-A1.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30888.
XX
PR 10-NOV-1999; 99US-0437458.
XX
PA (MESS-) MESSAGE PHARM INC.
XX
PI Giordano A, Xavier AK;
XX
DR WPI; 2001-335904/35.
XX
PT New nucleic acids that bind RNA-binding proteins or regulate mRNA
PT function, useful for therapeutic gene regulation, such as in cases of
PT neurodegeneration -
XX
PS Claim 1; Page 28; 33pp; English.
XX
CC Sequences AAH27132 - AAH27151 represent human gene untranslated regions

```
CC   where the corresponding mRNA fragment has RNA binding protein (RBP)
CC   binding activity. RBPs mediate the processing of pre-mRNA, the transport
CC   of mRNA from the nucleus to the cytoplasm, mRNA stabilisation,
CC   translational efficiency, and the sequestration of some mRNAs. Therefore
CC   modification of post-transcriptional protein expression in eukaryotic
CC   cells may be carried out through the targeting specific interactions of
CC   proteins that bind to RBPs. The gene fragments of the invention are used
CC   to identify their optimized sub-fragments, compounds that affect RNA/RBP
CC   interaction or mRNA functionality; or RBPs that interact with the
CC   compounds. Compounds identified using the gene fragments are potentially
CC   useful for therapeutic regulation of gene expression, such as in cases of
CC   neurodegeneration; stroke; cardiovascular disease; hypertension; cancer;
CC   inflammation; metabolic disorders (obesity and diabetes) and bacterial or
CC   viral infection. The present sequence is one of gene fragments of the
CC   invention, isolated from the human beta-2 adrenergic receptor gene.
XX
SQ   Sequence 230 BP; 42 A; 91 C; 70 G; 27 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 22;  Length 230;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||||||||||||||||||
Db     191 GGCTGGGGGCGCCTCAGCGG 172


RESULT 4
AAT93250/c
ID   AAT93250 standard; cDNA to mRNA; 1999 BP.
XX
AC   AAT93250;
XX
DT   20-APR-1998  (first entry)
XX
DE   Beta-2 adrenalin receptor subtype coding sequence.
XX
KW   Beta-2 adrenalin subtype; cyanopindrol; agonist; antagonist;
KW   asthmatic disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             190..1431
FT                   /*tag= a
XX
PN   WO9735963-A1.
XX
PD   02-OCT-1997.
XX
PF   24-MAR-1997;    97WO-JP00982.
XX
PR   27-MAR-1996;    96JP-0072914.
XX
PA   (DAIN ) DAINIPPON PHARM CO LTD.
XX
PI   Fujii K,  Furutani Y,  Kawashima H,  Nomura A,  Yano K;
XX
DR   WPI; 1997-489627/45.
DR   P-PSDB; AAW34320.
XX
PT   Novel beta-2 adrenalin receptor sub-type - useful for screening for
PT   agonists and antagonists and researching asthmatic diseases
XX
PS   Disclosure; Page 27-30; 47pp; Japanese.
XX
CC   This sequence encodes the protein of the invention. The protein of the
CC   invention is a beta-2 adrenalin receptor subtype with Kd value of
CC   approximately 75 pM against 125I-cyanopindrol. The protein can be used in
CC   screening for agonists and antagonists, which are useful in researching
CC   asthmatic diseases.
XX
SQ   Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 18;  Length 1999;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||||||||||||||||||
Db     161 GGCTGGGGGCGCCTCAGCGG 142


RESULT 5
AAA38784/c
ID   AAA38784 standard; DNA; 2340 BP.
XX
AC   AAA38784;
XX
DT   05-OCT-2000  (first entry)
XX
DE   Human beta2 adrenergic receptor beta2AR gene.
XX
KW   Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW   chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW   congestive heart failure; ischemic heart disease; arrhythmia;
KW   obesity; diabetes; vascular disease; premature labour; migraine;
KW   anaphylaxis; chronic obstructive pulmonary disease; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1487..2340
FT                   /*tag= a
FT                   /product= "beta2 adrenergic receptor"
FT                   /note= "no stop codon given at 3' end of sequence"
FT                   /partial
FT   sig_peptide     1487..1546
FT                   /*tag= b
FT                   /label= 5'_leader_cistron
FT   allele          replace(1541,T)
FT                   /*tag= c
FT   mat_peptide     1588..2340
FT                   /*tag= d
XX
PN   WO200031307-A1.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;    99WO-US27963.
XX
PR   25-NOV-1998;    98US-0109886.
XX
PA   (UYCI-) UNIV CINCINNATI.
XX
PI   Liggett SB;
XX
DR   WPI; 2000-400107/34.
XX
PT   Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT   receptor (beta 2 AR), useful for predicting genetic disposition to a
PT   disease modified by beta 2 AR expression e.g. congestive heart failure,
PT   hypertension -
XX
PS   Disclosure; Figure 1; 56pp; English.
XX
CC   The present sequence is a fragment of the C allele of the human beta2
CC   adrenergic receptor (beta2AR) gene, which is located on chromosome
CC   5q31 (12). The gene has two different alleles, and it has been shown that
CC   the presence of two copies of the T allele leads to higher expression of
CC   the gene. This is because the polymorphism is found in the 5' leader
CC   sequence, which encodes a peptide which regulates expression of the
CC   beta2AR gene. The polymorphism is thought to affect individuals'
CC   responses to beta-agonists and beta-antagonists, and is likely to
CC   influence their predisposition to asthma, hypertension,
CC   congestive heart failure, ischemic heart disease, arrhythmia, obesity,
```

```
CC   diabetes, vascular disease, premature labour, migraine, anaphylaxis and
CC   chronic obstructive pulmonary disease (COPD). The gene can, therefore, be
CC   used to predict the susceptibility of an individual to these diseases and
CC   determine the best treatment.
XX
SQ   Sequence 2340 BP; 498 A; 627 C; 653 G; 562 T; 0 other;

  Query Match           100.0%;  Score 20;  DB 21;  Length 2340;
  Best Local Similarity  100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCGG 20
          ||||||||||||||||||||
Db   1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 6
AAV52614/c
ID   AAV52614 standard; cDNA; 3451 BP.
XX
AC   AAV52614;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Human beta-2-adrenergic receptor cDNA.
XX
KW   Beta-2-adrenergic receptor; human; asthma; beta-agonist;
KW   polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1588..2829
FT                   /*tag=  a
FT   variation       1633
FT                   /*tag=  b
FT                   /note= "A to G substitution, results in Arg16
FT                          to Gly amino acid change"
XX
PN   WO9839477-A2.
XX
PD   11-SEP-1998.
XX
PF   26-FEB-1998;   98WO-US03908.
XX
PR   03-MAR-1997;   97US-0811441.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Boushey H,  Chinchilli VM,  Drazen JM,  Fish JE,  Ford JG;
PI   Martin RJ;
XX
DR   WPI; 1998-506372/43.
DR   P-PSDB; AAW75777.
XX
PT   Diagnosing asthma patients predisposed to adverse beta-agonist
PT   reactions upon regular administration - by identifying patients
PT   homozygous for allele encoding Arg at position 16 of
PT   beta2-adrenergic receptor protein
XX
PS   Disclosure; Page 33-35; 46pp; English.
XX
CC   This cDNA sequence codes for human beta-2-adrenergic receptor (see
CC   AAW75777) having an arginine residue at position 16.  A novel method
CC   for identifying individuals susceptible to adverse responses to
CC   regular administration of beta-agonists comprises: (a) identifying
CC   in a genomic nucleic acid sample from the individual first and
CC   second alleles of the beta 2-adrenergic receptor gene, and (b)
CC   classifying an individual as susceptible if first and second
CC   alleles both encode Arg at residue 16 of the beta 2-adrenergic
CC   receptor protein.  Beta 2-adrenergic receptor gene alleles may be
CC   identified by any known method e.g. denaturing gel electrophoresis
CC   or PCR amplification (see also AAV52615-17).  Identification
CC   preferably comprises amplifying a portion of each allele which
CC   includes the sequence encoding residue 16, and optionally also
CC   comprises determining nucleotide sequences of these portions (e.g.
CC   by automated sequence analysis).  The invention identifies a known
CC   polymorphism in the beta 2-adrenergic receptor gene as being linked
CC   to adverse responses to regular beta-agonist administration;
CC   position 16 of the encoded protein can be either Arg or Gly, and
CC   individuals homozygous for Arg16 are more susceptible.
XX
SQ   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

  Query Match           100.0%;  Score 20;  DB 19;  Length 3451;
  Best Local Similarity  100.0%;  Pred. No. 9.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGCTGGGGGCGCCTCAGCGG 20
          ||||||||||||||||||||
Db   1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 7
AAZ00776/c
ID   AAZ00776 standard; DNA; 3451 BP.
XX
AC   AAZ00776;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 3.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1633,a)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
FT   mutation        replace(1666,c)
FT                   /*tag=  b
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Glu
FT                          residue to Gln residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
```

```
PT   determining an individuals haplotype
XX
PS   Claim 4; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 789 A; 872 C; 897 G; 893 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 9.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 8
AAZ00779/c
ID   AAZ00779 standard; DNA; 3451 BP.
XX
AC   AAZ00779;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 6.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1568,t)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1633,a)
FT                   /*tag=  b
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
FT   mutation        replace(1666,c)
FT                   /*tag=  c
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Glu
FT                          residue to Gln residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 7; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 789 A; 873 C; 897 G; 892 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 9.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 9
AAZ00773/c
ID   AAZ00773 standard; DNA; 3451 BP.
XX
AC   AAZ00773;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor wild type DNA.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
```

```
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(159,a)
FT                   /*tag= a
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation       replace(245,g)
FT                   /*tag= b
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation       replace(565,a)
FT                   /*tag= c
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation       replace(934,a)
FT                   /*tag= d
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation       replace(1120,c)
FT                   /*tag= e
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation       replace(1221,t)
FT                   /*tag= f
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation       replace(1541,t)
FT                   /*tag= g
FT                   /note= "This mutation results in a change in the
FT                          corresponding wild type amino acid sequence
FT                          from an Arg residue to Cys residue in the
FT                          variant sequences represented in AAZ00774,
FT                          AAZ00775, AAZ00777, AAZ00778 and AAZ00780"
FT   mutation        replace(1568,c)
FT                   /*tag= h
FT                   /note= "This nucleotide differs from the wild type
FT                          in the variant nucleotide sequences represented
FT                          in AAZ00774 and AAZ00779"
FT   mutation        replace(1633,g)
FT                   /*tag= i
FT                   /note= "This mutation results in a change in the
FT                          corresponding wild type amino acid sequence
FT                          from an Arg residue to Gly residue in the
FT                          variant sequences represented in AAZ00774,
FT                          AAZ00776, AAZ00777, AAZ00779 and AAZ00780"
FT   mutation        replace(1666,g)
FT                   /*tag= j
FT                   /note= "This mutation results in a change in the
FT                          corresponding wild type amino acid sequence
FT                          from a Gln residue to Glu residue in the
FT                          variant sequences represented in AAZ00774,
FT                          AAZ00776, AAZ00779"
FT   mutation        replace(1839,a)
FT                   /*tag= k
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation       replace(2078,t)
FT                   /*tag= l
FT                   /note= "This mutation results in a change in the
FT                          corresponding wild type amino acid sequence
FT                          from a Thr residue to Ile residue"
FT   mutation        replace(2110,a)
FT                   /*tag= m
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation       replace(2640,c)
FT                   /*tag= n
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation       replace(2826,a)
FT                   /*tag= o
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT                          AAZ00774"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Disclosure; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be determined
CC   include neuropsychiatric disease, such as depression, anxiety, attention
CC   deficit disorder with hyperactivity, eating disorders, e.g. anorexia
CC   nervosa and bulimia, or post-traumatic stress disorder. Diseases of the
CC   autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and
CC   Riley-Day syndromes having selective noradrenergic-receptor disposition,
CC   or migraine, allergic conditions, e.g. asthma and atopic disorders, and
CC   metabolic illnesses, e.g. morbid obesity including predicting a change in
CC   weight, using body mass index, can also be determined. The beta
CC   2-adrenergic receptor sequence variants can be used to develop
CC   therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor
CC   agonists can be developed. Treatments can be optimized for individuals,
CC   including gene therapy and pharmaceutical intervention therapy. This
CC   sequence represents the wild type human beta 2-adrenergic receptor
CC   gene which is described in the method of the invention.
XX
SQ   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

  Query Match            100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity  100.0%;  Pred. No. 9.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           ||||||||||||||||||||
Db    1559 GGCTGGGGGCGCCTCAGCGG 1540


RESULT 10
AAA38339/c
ID   AAA38339 standard; DNA; 3451 BP.
XX
AC   AAA38339;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human beta-adrenergic receptor-2 gene regulatory region.
XX
KW   Beta-adrenergic receptor-2 gene; regulatory region;
KW   polymorphism; polymorphic marker; cardiovascular disease;
KW   myocardial infarction; unstable angina; hypertension; atherosclerosis;
KW   stroke; prognosis; drug screening; treatment outcome; human; ds.
XX
OS   Homo sapiens.
XX
```

PN WO200022166-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-IB01678.
XX
PR 14-OCT-1998; 98US-0104286.
PR 14-OCT-1998; 98US-0104302.
XX
PA (EURO-) EURONA MEDICAL AB.
XX
PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
XX
DR WPI; 2000-318010/27.
XX
PT Assessing cardiovascular status in humans involves comparing test
PT polymorphic pattern comprising polymorphic positions within genes
PT encoding specific proteins, with reference polymorphic pattern -
XX
PS Disclosure; Page 123-124; 126pp; English.
XX
CC The invention relates to a novel method of assessing the cardiovascular
CC status in an individual and to newly identified polymorphisms in the
CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II
CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
CC aldosterone synthase, endothelin receptor type A and beta-adrenergic
CC receptors 1 and 2. The method comprises determining the sequence at one
CC or more polymorphic positions within these genes, and comparing the
CC pattern of polymorphisms from the individual with a reference polymorphic
CC pattern obtained from a population of individuals exhibiting a
CC predetermined cardiovascular disease status. The polymorphic markers are
CC useful for determining the predisposition of an individual to
CC cardiovascular disorders such as myocardial infarction, unstable angina,
CC hypertension, atherosclerosis and stroke. They are also useful for
CC predicting the likely cardiovascular status of a patient given a
CC treatment regimen comprising administration of cardiovascular drugs
CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
CC blockers) or calcium channel blockers). One or more polymorphic markers
CC provides a basis for predicting the outcome of a treatment regimen.
CC Fragments of the genes comprising a polymorphic site may be used as
CC primers and probes for detecting genetic polymorphisms or in molecular
CC library arrays for high throughput screening. The genes, and the proteins
CC they encode are useful in the screening of potential cardiovascular
CC drugs. Determination of an individual's polymorphic pattern reduces or
CC eliminates trial and error in selecting a treatment for a particular
CC individual cardiovascular patient. It also provides the ability to
CC eliminate patients from clinical trials who are predicted to be
CC non-responsive, or at a risk for an adverse response, to a particular
CC treatment regimen. Adverse results in an early trial can be evaluated to
CC identify polymorphic patterns so that the adverse results can be
CC correlated with a sub-population of the test population, permitting
CC exclusion of such sub-populations from the treatment group. Beneficial
CC drugs can be approved for use in the appropriate population, thereby
CC decreasing the number of patients required for a clinical trial, which in
CC turn decreases the duration and cost of such trials. The present
CC sequence represents the human beta-adrenergic receptor-2 gene
CC regulatory region (GenBank M15169, J02728, M16106). The polymorphic
CC sites identified are 934A/G, 987C/G, 1006A/G, 1120C/G, 1221C/T,
CC 1541C/T and 1568C/T.
XX
SQ Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3451;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGGGCGCCTCAGCGG 20
||||||||||||||||||||
Db 1559 GGCTGGGGGCGCCTCAGCGG 1540

RESULT 11
AAS18444/c

ID AAS18444 standard; DNA; 3451 BP.
XX
AC AAS18444;
XX
DT 12-MAR-2002 (first entry)
XX
DE Reference sequence for human beta2AR gene showing polymorphisms.
XX
KW Human; beta2-adrenergic receptor; beta2AR polymorphism; asthma;
KW chromosome 5q31-32; migraine; congestive heart failure; hypertension;
KW ischaemic heart disease; chronic obstructive pulmonary disease; COPD;
KW obesity; diabetes mellitus; premature labour; vasotropic; cardiant;
KW antiarrhythmic; antiasthmatic; antidiabetic; tocolytic; ds.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	variation	replace (565, A)
FT		/*tag= a
FT		/note= "Polymorphic site 1 (PS1)"
FT	variation	replace (879, A)
FT		/*tag= b
FT		/note= "Polymorphic site 2 (PS2)"
FT	variation	replace (934, A)
FT		/*tag= c
FT		/note= "Polymorphic site 3 (PS3)"
FT	variation	replace (1120, C)
FT		/*tag= d
FT		/note= "Polymorphic site 4 (PS4)"
FT	variation	replace (1182, T)
FT		/*tag= e
FT		/note= "Polymorphic site 5 (PS5)"
FT	variation	replace (1221, T)
FT		/*tag= f
FT		/note= "Polymorphic site 6 (PS6)"
FT	variation	replace (1541, T)
FT		/*tag= g
FT		/note= "Polymorphic site 7 (PS7)"
FT	variation	replace (1568, C)
FT		/*tag= h
FT		/note= "Polymorphic site 8 (PS8)"
FT	CDS	1588..2829
FT		/*tag= i
FT		/product= "Beta2AR"
FT	variation	replace (1633, G)
FT		/*tag= j
FT		/note= "Polymorphic site 9 (PS9)"
FT	variation	replace (1666, G)
FT		/*tag= k
FT		/note= "Polymorphic site 10 (PS10)"
FT	variation	replace (1839, A)
FT		/*tag= l
FT		/note= "Polymorphic site 11 (PS11)"
FT	variation	replace (2078, T)
FT		/*tag= m
FT		/note= "Polymorphic site 12 (PS12)"
FT	variation	replace (2110, A)
FT		/*tag= n
FT		/note= "Polymorphic site 13 (PS13)"

XX
PN WO200179252-A1.
XX
PD 25-OCT-2001.
XX
PF 13-APR-2000; 2000WO-US10125.
XX
PR 13-APR-2000; 2000WO-US10125.
XX
PA (GENA-) GENAISSANCE PHARM INC.
PA (UYCI-) UNIV CINCINNATI.
XX
PI Stack CB, Drysdale CM, Stephens JC, Nandabalan K, Judson RS;
PI Liggett SB;

XX
DR WPI; 2002-061968/08.
DR P-PSDB; AAU10763.
XX
PT New isolated beta 2-adrenergic receptor polynucleotide, useful for
PT studying expression and biological function of receptor and for
PT developing drugs targeting receptor, comprises polymorphism of
PT adenosine at PS2 and thymine at PS5 -
XX
PS Claim 1; Fig 1; 67pp; English.
XX
CC The present invention relates to polymorphisms and haplotypes of
CC the human beta2-adrenergic receptor (beta2-AR) gene located on
CC chromosome 5q31-32, and methods for haplotyping and/or genotyping the
CC beta2AR gene in an individual. The methods of the invention make use of
CC allele-specific oligonucleotides (ASOs) as probes and primers for
CC detecting the beta2AR gene polymorphisms. The beta2AR gene polymorphisms
CC are useful in studying the expression and biological function of beta2AR,
CC and for developing drugs targeting this receptor. They are also useful
CC for therapeutic purposes such as treating disorders affected by
CC expression or function of beta2AR such as congestive heart failure,
CC arrhythmia, ischaemic heart disease, hypertension, migraine, asthma,
CC chronic obstructive pulmonary disease (COPD), obesity, diabetes and
CC premature labour. The method is useful for determining the frequency of
CC a beta2AR genotype or haplotype in a population. The present sequence
CC represents a reference sequence for the human beta2AR gene which shows
CC the polymorphisms in the gene.
XX
SQ Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 3451;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGGGCGCCTCAGCGG 20
||||||||||||||||||||
Db 1559 GGCTGGGGGCGCCTCAGCGG 1540

RESULT 12
AAA46130
ID AAA46130 standard; DNA; 20 BP.
XX
AC AAA46130;
XX
DT 05-OCT-2000 (first entry)
XX
DE Human beta2 adrenergic receptor beta2AR T allele-specific primer #2.
XX
KW Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW congestive heart failure; ischemic heart disease; arrhythmia;
KW obesity; diabetes; vascular disease; premature labour; migraine;
KW anaphylaxis; chronic obstructive pulmonary disease;
KW allele-specific oligonucleotide primer; ss.
XX
OS Homo sapiens.
XX
PN WO200031307-A1.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US27963.
XX
PR 25-NOV-1998; 98US-0109886.
XX
PA (UYCI-) UNIV CINCINNATI.
XX
PI Liggett SB;
XX
DR WPI; 2000-400107/34.
XX
PT Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT receptor (beta 2 AR), useful for predicting genetic disposition to a
PT disease modified by beta 2 AR expression e.g. congestive heart failure,
PT hypertension -
XX
PS Claim 8; Page 12; 56pp; English.
XX
CC The present sequence is an allele-specific oligonucleotide primer
CC for the T allele of the human beta2 adrenergic receptor (beta2AR) gene,
CC which is located on chromosome 5q31 (12). The gene has two different
CC alleles, and it has been shown that the presence of two copies of the T
CC allele leads to higher expression of the gene. This is because the
CC polymorphism is found in the 5' leader sequence, which encodes a peptide
CC which regulates expression of the beta2AR gene. The polymorphism is
CC thought to affect individuals' responses to beta-agonists and
CC beta-antagonists, and is likely to influence their predisposition to
CC asthma, hypertension, congestive heart failure, ischemic heart disease,
CC arrhythmia, obesity, diabetes, vascular disease, premature labour,
CC migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD).
CC The gene can, therefore, be used to predict the susceptibility of an
CC individual to these diseases and determine the best treatment.
XX
SQ Sequence 20 BP; 2 A; 6 C; 10 G; 2 T; 0 other;

Query Match 92.0%; Score 18.4; DB 21; Length 20;
Best Local Similarity 95.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGCTGGGGGCGCCTCAGCGG 20
||||||||||||||||||| |
Db 1 GGCTGGGGGCGCCTCAGCAG 20

RESULT 13
AAX61116/c
ID AAX61116 standard; DNA; 2300 BP.
XX
AC AAX61116;
XX
DT 27-JUL-1999 (first entry)
XX
DE Human beta2-adrenergic receptor gene.
XX
KW Alpha1B-adrenergic receptor; human; cardiovascular disease;
KW beta2 adrenergic receptor; genetic variation identification; hypertrophy;
KW disease diagnosis; hypertension; prostatic disease; pulmonary disorder;
KW asthma; peripheral vascular disorder; neuropsychic disorder;
KW endocrine-metabolic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO9924454-A1.
XX
PD 20-MAY-1999.
XX
PF 04-NOV-1998; 98WO-US23496.
XX
PR 10-NOV-1997; 97US-0086232.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Buescher R, Herrmann V, Insel PA;
XX
DR WPI; 1999-327357/27.
XX
PT Pairs of oligonucleotides for amplifying adrenergic receptor genes
XX
PS Disclosure; Fig 2; 58pp; English.
XX
CC This sequence represents the human beta2-adrenergic receptor gene, and
CC is amplified by the primers of the invention. The primers are non-self
CC hybridising; contain at least 15 nucleotides (nt) and has a melting
CC temperature 50-85 deg. C. Each pair of primers is: non-cross-hybridising;
CC anneals to two distinct segments (separated by at least 400 nt); and

CC generates a homogeneous population of gene segments in a polymerase chain
CC reaction (PCR). At least one primer in the pair can extend a 3'-end
CC sequence complementary to a template sequence in a DNA polymerase
CC reaction. The primers are used to amplify segments of the alpha1B and
CC beta2 adrenergic receptor genes, particularly to identify genetic
CC variations for diagnosis of disease. Specifically variations in the
CC alpha1B gene are associated with cardiovascular disease, hypertension and
CC prostatic disease (hypertrophy), and those in the beta2 gene with
CC cardiovascular disease, hypertension and asthma, but variations may also
CC be associated with peripheral vascular, pulmonary, neuropsychic and
CC endocrine-metabolic disorders. These primers allow rapid and specific
CC amplification of large and homogeneous gene segments of the alpha1B and
CC beta2 genes from a complex mixture of DNAs. This makes possible detection
CC of genetic alterations not previously amenable to routine, automated and
CC large-scale sequencing analysis.
XX
SQ Sequence 2300 BP; 495 A; 613 C; 646 G; 546 T; 0 other;

Query Match 92.0%; Score 18.4; DB 20; Length 2300;
Best Local Similarity 95.0%; Pred. No. 46;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGCTGGGGGCGCCTCAGCGG 20
||||||||||||||||||| |
Db 765 GGCTGGGGGCGCCTCAGCAG 746

RESULT 14
AAA38340/c
ID AAA38340 standard; DNA; 2305 BP.
XX
AC AAA38340;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human beta-adrenergic receptor-2 coding region.
XX
KW Beta-adrenergic receptor-2 gene; coding region;
KW polymorphism; polymorphic marker; cardiovascular disease;
KW myocardial infarction; unstable angina; hypertension; atherosclerosis;
KW stroke; prognosis; drug screening; treatment outcome; human; ds.
XX
OS Homo sapiens.
XX
PN WO200022166-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-IB01678.
XX
PR 14-OCT-1998; 98US-0104286.
PR 14-OCT-1998; 98US-0104302.
XX
PA (EURO-) EURONA MEDICAL AB.
XX
PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
XX
DR WPI; 2000-318010/27.
XX
PT Assessing cardiovascular status in humans involves comparing test
PT polymorphic pattern comprising polymorphic positions within genes
PT encoding specific proteins, with reference polymorphic pattern -
XX
PS Disclosure; Page 124-125; 126pp; English.
XX
CC The invention relates to a novel method of assessing the cardiovascular
CC status in an individual and to newly identified polymorphisms in the
CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II
CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
CC aldosterone synthase, endothelin receptor type A and beta-adrenergic
CC receptors 1 and 2. The method comprises determining the sequence at one
CC or more polymorphic positions within these genes, and comparing the
CC pattern of polymorphisms from the individual with a reference polymorphic
CC pattern obtained from a population of individuals exhibiting a
CC predetermined cardiovascular disease status. The polymorphic markers are
CC useful for determining the predisposition of an individual to
CC cardiovascular disorders such as myocardial infarction, unstable angina,
CC hypertension, atherosclerosis and stroke. They are also useful for
CC predicting the likely cardiovascular status of a patient given a
CC treatment regimen comprising administration of cardiovascular drugs
CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
CC blockers) or calcium channel blockers). One or more polymorphic markers
CC provides a basis for predicting the outcome of a treatment regimen.
CC Fragments of the genes comprising a polymorphic site may be used as
CC primers and probes for detecting genetic polymorphisms or in molecular
CC library arrays for high throughput screening. The genes, and the proteins
CC they encode are useful in the screening of potential cardiovascular
CC drugs. Determination of an individual's polymorphic pattern reduces or
CC eliminates trial and error in selecting a treatment for a particular
CC individual cardiovascular patient. It also provides the ability to
CC eliminate patients from clinical trials who are predicted to be
CC non-responsive, or at a risk for an adverse response, to a particular
CC treatment regimen. Adverse results in an early trial can be evaluated to
CC identify polymorphic patterns so that the adverse results can be
CC correlated with a sub-population of the test population, permitting
CC exclusion of such sub-populations from the treatment group. Beneficial
CC drugs can be approved for use in the appropriate population, thereby
CC decreasing the number of patients required for a clinical trial, which in
CC turn decreases the duration and cost of such trials. The present
CC sequence represents the human beta-adrenergic receptor-2 gene
CC coding region (GenBank Y00106/g293708). The polymorphic sites identified
CC are 839A/G, 872C/G, 1045A/G, 1284C/T, 1316A/C, 1846C/G, 2032A/G,
CC 2068 no insert/G/C and 2070 no insert/C.
XX
SQ Sequence 2305 BP; 495 A; 616 C; 649 G; 545 T; 0 other;

Query Match 92.0%; Score 18.4; DB 21; Length 2305;
Best Local Similarity 95.0%; Pred. No. 46;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGCTGGGGGCGCCTCAGCGG 20
||||||||||||||||||| |
Db 765 GGCTGGGGGCGCCTCAGCAG 746

RESULT 15
AAZ00774/c
ID AAZ00774 standard; DNA; 3451 BP.
XX
AC AAZ00774;
XX
DT 07-OCT-1999 (first entry)
XX
DE Human beta 2-adrenergic receptor DNA variant 1.
XX
KW Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW cardiovascular disease; myocardial infarction; anxiety; depression;
KW neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW post-traumatic stress disorder; autonomous nervous system disease;
KW metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation replace(159,t)
FT /*tag= a
FT /note= "This nucleotide differs from the wild type
FT nucleic acid sequence represented in AAZ00773"
FT mutation replace(245,a)
FT /*tag= b
FT /note= "This nucleotide differs from the wild type
FT nucleic acid sequence represented in AAZ00773"

```
FT   mutation        replace(565,g)
FT                   /*tag= c
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(934,g)
FT                   /*tag= d
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1120,g)
FT                   /*tag= e
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1221,c)
FT                   /*tag= f
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1541,t)
FT                   /*tag= g
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Cys
FT                          residue to Arg residue"
FT   mutation        replace(1568,t)
FT                   /*tag= h
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1633,a)
FT                   /*tag= i
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
FT   mutation        replace(1666,c)
FT                   /*tag= j
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Glu
FT                          residue to Gln residue"
FT   mutation        replace(1839,g)
FT                   /*tag= k
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(2078,c)
FT                   /*tag= l
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Ile
FT                          residue to Thr residue"
FT   mutation        replace(2110,c)
FT                   /*tag= m
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(2640,g)
FT                   /*tag= n
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(2826,g)
FT                   /*tag= o
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 2; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 794 A; 871 C; 892 G; 894 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 20;  Length 3451;
  Best Local Similarity   95.0%;  Pred. No. 45;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCTGGGGGCGCCTCAGCGG 20
           |||||||||||||||||| |
Db    1559 GGCTGGGGGCGCCTCAGCAG 1540


Search completed: November  2, 2002, 16:13:18
Job time : 84.7273 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 13:09:44 ; Search time 82.7273 Seconds
(without alignments)
415.078 Million cell updates/sec

Title: US-09-856-803-7
Perfect score: 20
Sequence: 1 ccccgccgtgggtccgcccg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
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2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	21	AAA38788	Human beta2 adrene
2	20	100.0	51	22	AAH79739	Human DNA containi
3	20	100.0	230	22	AAH27139	Human beta-2 adren
4	20	100.0	1999	18	AAT93250	Beta-2 adrenalin r
5	20	100.0	2340	21	AAA38784	Human beta2 adrene
6	20	100.0	3451	19	AAV52614	Human beta-2-adren
7	20	100.0	3451	20	AAZ00776	Human beta 2-adren
8	20	100.0	3451	20	AAZ00779	Human beta 2-adren
9	20	100.0	3451	20	AAZ00773	Human beta 2-adren
10	20	100.0	3451	21	AAA38339	Human beta-adrener
11	20	100.0	3451	24	AAS18444	Reference sequence
12	18.4	92.0	20	21	AAA46128	Human beta2 adrene
13	18.4	92.0	60	21	AAA38785	Human beta2 adrene
14	18.4	92.0	2300	20	AAX61116	Human beta2-adrene
15	18.4	92.0	2305	21	AAA38340	Human beta-adrener
16	18.4	92.0	3451	20	AAZ00774	Human beta 2-adren
17	18.4	92.0	3451	20	AAZ00775	Human beta 2-adren
18	18.4	92.0	3451	20	AAZ00777	Human beta 2-adren
19	18.4	92.0	3451	20	AAZ00778	Human beta 2-adren
20	18.4	92.0	3451	20	AAZ00780	Human beta 2-adren
21	16.8	84.0	1400	18	AAT93249	Beta-2 adrenalin r
c 22	16.4	82.0	1770	22	AAF30281	Perilla flavone sy
c 23	16	80.0	675	23	ABL13277	Drosophila melanog
c 24	16	80.0	8100	23	ABL13276	Drosophila melanog
c 25	15.8	79.0	292	21	AAC07659	Human secreted pro
c 26	15.8	79.0	320	22	AAS59448	Human KCC4 genomic
c 27	15.8	79.0	624	22	AAK61432	Human immune/haema
c 28	15.8	79.0	739	21	AAZ38854	Human Jurkat cell
c 29	15.8	79.0	882	21	AAC75955	Human ORFX ORF1510
30	15.8	79.0	1052	22	AAS29788	Human cytoskeletal
c 31	15.8	79.0	10934	22	AAS13494	Mouse VMGLOM genom
32	15.8	79.0	12488	19	AAV62132	HSV-2 strain SB5 C
c 33	15.8	79.0	14806	22	AAD03809	Streptomyces galil
c 34	15.8	79.0	21034	19	AAV62154	HSV-2 strain SB5 C
35	15.8	79.0	73947	23	ABL07230	Drosophila melanog
c 36	15.8	79.0	117213	19	AAV62176	HSV-2 strain SB5 C
c 37	15.8	79.0	154746	24	AAD25519	Human herpesvirus
38	15.4	77.0	4100	16	AAQ74062	The rat beta-actin
c 39	15.4	77.0	65632	21	AAA81502	N. meningitidis pa
40	15.4	77.0	349980	21	AAF21544	Neisseria meningit
41	15.4	77.0	1437668	21	AAA81490	N. meningitidis B
c 42	15.2	76.0	40	18	AAT98479	Template switching
c 43	15.2	76.0	40	18	AAT98480	Template switching
c 44	15.2	76.0	40	18	AAT98492	Template switching
c 45	15.2	76.0	40	20	AAZ28717	Oligonucleotide RT

ALIGNMENTS

RESULT 1
AAA38788
ID AAA38788 standard; DNA; 20 BP.
XX
AC AAA38788;
XX
DT 05-OCT-2000 (first entry)
XX
DE Human beta2 adrenergic receptor beta2AR C allele-specific primer #1.
XX
KW Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW congestive heart failure; ischemic heart disease; arrhythmia;
KW obesity; diabetes; vascular disease; premature labour; migraine;
KW anaphylaxis; chronic obstructive pulmonary disease;
KW allele-specific oligonucleotide primer; ss.
XX
OS Homo sapiens.
XX
PN WO200031307-A1.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US27963.
XX
PR 25-NOV-1998; 98US-0109886.
XX
PA (UYCI-) UNIV CINCINNATI.
XX
PI Liggett SB;
XX
DR WPI; 2000-400107/34.

```
XX
PT   Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT   receptor (beta 2 AR), useful for predicting genetic disposition to a
PT   disease modified by beta 2 AR expression e.g. congestive heart failure,
PT   hypertension -
XX
PS   Claim 8; Page 11; 56pp; English.
XX
CC   The present sequence is an allele-specific oligonucleotide primer
CC   for the C allele of the human beta2 adrenergic receptor (beta2AR) gene,
CC   which is located on chromosome 5q31 (12). The gene has two different
CC   alleles, and it has been shown that the presence of two copies of the T
CC   allele leads to higher expression of the gene. This is because the
CC   polymorphism is found in the 5' leader sequence, which encodes a peptide
CC   which regulates expression of the beta2AR gene. The polymorphism is
CC   thought to affect individuals' responses to beta-agonists and
CC   beta-antagonists, and is likely to influence their predisposition to
CC   asthma, hypertension, congestive heart failure, ischemic heart disease,
CC   arrhythmia, obesity, diabetes, vascular disease, premature labour,
CC   migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD).
CC   The gene can, therefore, be used to predict the susceptibility of an
CC   individual to these diseases and determine the best treatment.
XX
SQ   Sequence 20 BP; 0 A; 11 C; 7 G; 2 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db      1 CCCCGCCGTGGGTCCGCCCG 20


RESULT 2
AAH79739
ID   AAH79739 standard; DNA; 51 BP.
XX
AC   AAH79739;
XX
DT   19-SEP-2001  (first entry)
XX
DE   Human DNA containing single nucleotide polymorphism SEQ ID NO. 354.
XX
KW   Human; single nucleotide polymorphism; SNP; angiopoietin;
KW   4-hydroxybutyrate; dehydrogenase; protein therapy;
KW   adenosine triphosphate-dependent RNA helicase;
KW   major histocompatibility complex Class I histocompatibility antigen; MHC;
KW   phosphoglycerate kinase; immunosuppressive; immunostimulatory;
KW   antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
KW   antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; ds.
XX
OS   Homo sapiens.
XX
PN   WO200148245-A2.
XX
PD   05-JUL-2001.
XX
PF   27-DEC-2000; 2000WO-US35346.
XX
PR   27-DEC-1999;   99US-0472688.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-418297/44.
XX
PT   Polymorphic nucleic acids encoding e.g. angiopoietin, dehydrogenase,
PT   adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
PT   kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
PT   diseases and infections -
XX
PS   Claim 1; Page 162; 484pp; English.
XX
CC   The invention relates to nucleic acids (AAH79386-AAH80036) encoding
CC   polymorphic variants of proteins (AAG98010-AAG98238) related to
CC   angiopoietin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
CC   (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
CC   Class I histocompatibility antigen and/or phosphoglycerate kinase. These
CC   nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
CC   proteins have potential immunosuppressive, immunostimulatory,
CC   antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
CC   antileukemic, neuroprotective and antimicrobial activity and may be
CC   useful in gene/protein therapy, vaccines, modulation of the expression
CC   and activity of proteins related to angiopoietin, 4-hydroxybutyrate,
CC   dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase,
CC   major histocompatibility complex (MHC) Class I histocompatibility antigen
CC   and/or phosphoglycerate kinase. Disorders that may be prevented,
CC   diagnosed and/or treated by the above methods include multifactorial
CC   diseases with a genetic component, such as autoimmune diseases (e.g.
CC   rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
CC   erytheromatosus and Grave's disease), inflammation, cancer (e.g. cancers
CC   of the bladder, brain, breast, colon and kidney, leukemia), diseases of
CC   the nervous system, an infection of pathogenic organisms. They may also
CC   be used to alter phenotypic traits such as longevity, appearance,
CC   strength, speed and endurance.
XX
SQ   Sequence 51 BP; 5 A; 24 C; 18 G; 4 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 22;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db      8 CCCCGCCGTGGGTCCGCCCG 27


RESULT 3
AAH27139
ID   AAH27139 standard; DNA; 230 BP.
XX
AC   AAH27139;
XX
DT   08-AUG-2001  (first entry)
XX
DE   Human beta-2 adrenergic receptor UTR region with RBP binding ability.
XX
KW   Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration;
KW   stroke; cardiovascular disease; hypertension; cancer; inflammation;
KW   metabolic disorder; obesity; diabetes; beta-2 adrenergic receptor; ds.
XX
OS   Homo sapiens.
XX
PN   WO200134624-A1.
XX
PD   17-MAY-2001.
XX
PF   09-NOV-2000; 2000WO-US30888.
XX
PR   10-NOV-1999;   99US-0437458.
XX
PA   (MESS-) MESSAGE PHARM INC.
XX
PI   Giordano A,  Xavier AK;
XX
DR   WPI; 2001-335904/35.
XX
PT   New nucleic acids that bind RNA-binding proteins or regulate mRNA
PT   function, useful for therapeutic gene regulation, such as in cases of
PT   neurodegeneration  -
XX
PS   Claim 1; Page 28; 33pp; English.
XX
CC   Sequences AAH27132 - AAH27151 represent human gene untranslated regions
```

```
CC   where the corresponding mRNA fragment has RNA binding protein (RBP)
CC   binding activity. RBPs mediate the processing of pre-mRNA, the transport
CC   of mRNA from the nucleus to the cytoplasm, mRNA stabilisation,
CC   translational efficiency, and the sequestration of some mRNAs. Therefore
CC   modification of post-transcriptional protein expression in eukaryotic
CC   cells may be carried out through the targeting specific interactions of
CC   proteins that bind to RBPs. The gene fragments of the invention are used
CC   to identify their optimized sub-fragments, compounds that affect RNA/RBP
CC   interaction or mRNA functionality; or RBPs that interact with the
CC   compounds. Compounds identified using the gene fragments are potentially
CC   useful for therapeutic regulation of gene expression, such as in cases of
CC   neurodegeneration; stroke; cardiovascular disease; hypertension; cancer;
CC   inflammation; metabolic disorders (obesity and diabetes) and bacterial or
CC   viral infection. The present sequence is one of gene fragments of the
CC   invention, isolated from the human beta-2 adrenergic receptor gene.
XX
SQ   Sequence 230 BP; 42 A; 91 C; 70 G; 27 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 22;  Length 230;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCCG 20
           ||||||||||||||||||||
Db     155 CCCCGCCGTGGGTCCGCCCG 174


RESULT 4
AAT93250
ID   AAT93250 standard; cDNA to mRNA; 1999 BP.
XX
AC   AAT93250;
XX
DT   20-APR-1998  (first entry)
XX
DE   Beta-2 adrenalin receptor subtype coding sequence.
XX
KW   Beta-2 adrenalin subtype; cyanopindrol; agonist; antagonist;
KW   asthmatic disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             190..1431
FT                   /*tag=  a
XX
PN   WO9735963-A1.
XX
PD   02-OCT-1997.
XX
PF   24-MAR-1997;   97WO-JP00982.
XX
PR   27-MAR-1996;   96JP-0072914.
XX
PA   (DAIN ) DAINIPPON PHARM CO LTD.
XX
PI   Fujii K,  Furutani Y,  Kawashima H,  Nomura A,  Yano K;
XX
DR   WPI; 1997-489627/45.
DR   P-PSDB; AAW34320.
XX
PT   Novel beta-2 adrenalin receptor sub-type - useful for screening for
PT   agonists and antagonists and researching asthmatic diseases
XX
PS   Disclosure; Page 27-30; 47pp; Japanese.
XX
CC   This sequence encodes the protein of the invention. The protein of the
CC   invention is a beta-2 adrenalin receptor subtype with Kd value of
CC   approximately 75 pM against 125I-cyanopindrol. The protein can be used in
CC   screening for agonists and antagonists, which are useful in researching
CC   asthmatic diseases.
XX
SQ   Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 18;  Length 1999;
  Best Local Similarity   100.0%;  Pred. No. 8.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCCG 20
           ||||||||||||||||||||
Db     125 CCCCGCCGTGGGTCCGCCCG 144


RESULT 5
AAA38784
ID   AAA38784 standard; DNA; 2340 BP.
XX
AC   AAA38784;
XX
DT   05-OCT-2000  (first entry)
XX
DE   Human beta2 adrenergic receptor beta2AR gene.
XX
KW   Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW   chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW   congestive heart failure; ischemic heart disease; arrhythmia;
KW   obesity; diabetes; vascular disease; premature labour; migraine;
KW   anaphylaxis; chronic obstructive pulmonary disease; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1487..2340
FT                   /*tag=  a
FT                   /product= "beta2 adrenergic receptor"
FT                   /note= "no stop codon given at 3' end of sequence"
FT                   /partial
FT   sig_peptide     1487..1546
FT                   /*tag=  b
FT                   /label= 5'_leader_cistron
FT   allele          replace(1541,T)
FT                   /*tag=  c
FT   mat_peptide     1588..2340
FT                   /*tag=  d
XX
PN   WO200031307-A1.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US27963.
XX
PR   25-NOV-1998;   98US-0109886.
XX
PA   (UYCI-) UNIV CINCINNATI.
XX
PI   Liggett SB;
XX
DR   WPI; 2000-400107/34.
XX
PT   Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT   receptor (beta 2 AR), useful for predicting genetic disposition to a
PT   disease modified by beta 2 AR expression e.g. congestive heart failure,
PT   hypertension -
XX
PS   Disclosure; Figure 1; 56pp; English.
XX
CC   The present sequence is a fragment of the C allele of the human beta2
CC   adrenergic receptor (beta2AR) gene, which is located on chromosome
CC   5q31 (12). The gene has two different alleles, and it has been shown that
CC   the presence of two copies of the T allele leads to higher expression of
CC   the gene. This is because the polymorphism is found in the 5' leader
CC   sequence, which encodes a peptide which regulates expression of the
CC   beta2AR gene. The polymorphism is thought to affect individuals'
CC   responses to beta-agonists and beta-antagonists, and is likely to
CC   influence their predisposition to asthma, hypertension,
CC   congestive heart failure, ischemic heart disease, arrhythmia, obesity,
```

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CC   diabetes, vascular disease, premature labour, migraine, anaphylaxis and
CC   chronic obstructive pulmonary disease (COPD). The gene can, therefore, be
CC   used to predict the susceptibility of an individual to these diseases and
CC   determine the best treatment.
XX
SQ   Sequence 2340 BP; 498 A; 627 C; 653 G; 562 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 21;  Length 2340;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db   1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 6
AAV52614
ID   AAV52614 standard; cDNA; 3451 BP.
XX
AC   AAV52614;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Human beta-2-adrenergic receptor cDNA.
XX
KW   Beta-2-adrenergic receptor; human; asthma; beta-agonist;
KW   polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1588..2829
FT                   /*tag=  a
FT   variation       1633
FT                   /*tag=  b
FT                   /note= "A to G substitution, results in Arg16
FT                          to Gly amino acid change"
XX
PN   WO9839477-A2.
XX
PD   11-SEP-1998.
XX
PF   26-FEB-1998;   98WO-US03908.
XX
PR   03-MAR-1997;   97US-0811441.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Boushey H,  Chinchilli VM,  Drazen JM,  Fish JE,  Ford JG;
PI   Martin RJ;
XX
DR   WPI; 1998-506372/43.
DR   P-PSDB; AAW75777.
XX
PT   Diagnosing asthma patients predisposed to adverse beta-agonist
PT   reactions upon regular administration - by identifying patients
PT   homozygous for allele encoding Arg at position 16 of
PT   beta2-adrenergic receptor protein
XX
PS   Disclosure; Page 33-35; 46pp; English.
XX
CC   This cDNA sequence codes for human beta-2-adrenergic receptor (see
CC   AAW75777) having an arginine residue at position 16.  A novel method
CC   for identifying individuals susceptible to adverse responses to
CC   regular administration of beta-agonists comprises: (a) identifying
CC   in a genomic nucleic acid sample from the individual first and
CC   second alleles of the beta 2-adrenergic receptor gene, and (b)
CC   classifying an individual as susceptible if first and second
CC   alleles both encode Arg at residue 16 of the beta 2-adrenergic
CC   receptor protein.  Beta 2-adrenergic receptor gene alleles may be
CC   identified by any known method e.g. denaturing gel electrophoresis
CC   or PCR amplification (see also AAV52615-17).  Identification
CC   preferably comprises amplifying a portion of each allele which
CC   includes the sequence encoding residue 16, and optionally also
CC   comprises determining nucleotide sequences of these portions (e.g.
CC   by automated sequence analysis).  The invention identifies a known
CC   polymorphism in the beta 2-adrenergic receptor gene as being linked
CC   to adverse responses to regular beta-agonist administration;
CC   position 16 of the encoded protein can be either Arg or Gly, and
CC   individuals homozygous for Arg16 are more susceptible.
XX
SQ   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 19;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCCG 20
          ||||||||||||||||||||
Db   1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 7
AAZ00776
ID   AAZ00776 standard; DNA; 3451 BP.
XX
AC   AAZ00776;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 3.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1633,a)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                           nucleic acid sequence represented in AAZ00773
FT                           and results in a change in the corresponding
FT                           wild type amino acid sequence from an Gly
FT                           residue to Arg residue"
FT   mutation        replace(1666,c)
FT                   /*tag=  b
FT                   /note= "This nucleotide differs from the wild type
FT                           nucleic acid sequence represented in AAZ00773
FT                           and results in a change in the corresponding
FT                           wild type amino acid sequence from an Glu
FT                           residue to Gln residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
```

```
PT   determining an individuals haplotype
XX
PS   Claim 4; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 789 A; 872 C; 897 G; 893 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCCG 20
           ||||||||||||||||||||
Db    1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 8
AAZ00779
ID   AAZ00779 standard; DNA; 3451 BP.
XX
AC   AAZ00779;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor DNA variant 6.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1568,t)
FT                   /*tag=  a
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773"
FT   mutation        replace(1633,a)
FT                   /*tag=  b
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Gly
FT                          residue to Arg residue"
FT   mutation        replace(1666,c)
FT                   /*tag=  c
FT                   /note= "This nucleotide differs from the wild type
FT                          nucleic acid sequence represented in AAZ00773
FT                          and results in a change in the corresponding
FT                          wild type amino acid sequence from an Glu
FT                          residue to Gln residue"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Claim 7; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be
CC   determined include neuropsychiatric disease, such as depression, anxiety,
CC   attention deficit disorder with hyperactivity, eating disorders, e.g.
CC   anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
CC   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
CC   and Riley-Day syndromes having selective noradrenergic-receptor
CC   disposition, or migraine, allergic conditions, e.g. asthma and atopic
CC   disorders, and metabolic illnesses, e.g. morbid obesity including
CC   predicting a change in weight, using body mass index, can also be
CC   determined. The beta 2-adrenergic receptor sequence variants can be used
CC   to develop therapeutics and/or lifestyle drugs. Individual specific beta
CC   2-receptor agonists can be developed. Treatments can be optimized for
CC   individuals, including gene therapy and pharmaceutical intervention
CC   therapy. This sequence represents a variant of the wild type human beta
CC   2-adrenergic receptor gene which is represented in AAZ00773.
XX
SQ   Sequence 3451 BP; 789 A; 873 C; 897 G; 892 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCCG 20
           ||||||||||||||||||||
Db    1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 9
AAZ00773
ID   AAZ00773 standard; DNA; 3451 BP.
XX
AC   AAZ00773;
XX
DT   07-OCT-1999  (first entry)
XX
DE   Human beta 2-adrenergic receptor wild type DNA.
XX
KW   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
KW   neuroprotector; immunosuppressor; predisposition; high blood pressure;
KW   cardiovascular disease; myocardial infarction; anxiety; depression;
KW   neuropsychiatric disease; attention deficit disorder; hyperactivity;
KW   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
KW   post-traumatic stress disorder; autonomous nervous system disease;
KW   metabolic illness; gene therapy; pharmaceutical intervention therapy;
```

```
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(159,a)
FT                   /*tag= a
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation      replace(245,g)
FT                   /*tag= b
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation      replace(565,a)
FT                   /*tag= c
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation      replace(934,a)
FT                   /*tag= d
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation      replace(1120,c)
FT                   /*tag= e
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation      replace(1221,t)
FT                   /*tag= f
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation      replace(1541,t)
FT                   /*tag= g
FT                   /note= "This mutation results in a change in the
FT                          corresponding wild type amino acid sequence
FT                          from an Arg residue to Cys residue in the
FT                          variant sequences represented in AAZ00774,
FT                          AAZ00775, AAZ00777, AAZ00778 and AAZ00780"
FT   mutation        replace(1568,c)
FT                   /*tag= h
FT                   /note= "This nucleotide differs from the wild type
FT                          in the variant nucleotide sequences represented
FT                          in AAZ00774 and AAZ00779"
FT   mutation        replace(1633,g)
FT                   /*tag= i
FT                   /note= "This mutation results in a change in the
FT                          corresponding wild type amino acid sequence
FT                          from an Arg residue to Gly residue in the
FT                          variant sequences represented in AAZ00774,
FT                          AAZ00776, AAZ00777, AAZ00779 and AAZ00780"
FT   mutation        replace(1666,g)
FT                   /*tag= j
FT                   /note= "This mutation results in a change in the
FT                          corresponding wild type amino acid sequence
FT                          from a Gln residue to Glu residue in the
FT                          variant sequences represented in AAZ00774,
FT                          AAZ00776, AAZ00779"
FT   mutation        replace(1839,a)
FT                   /*tag= k
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation      replace(2078,t)
FT                   /*tag= l
FT                   /note= "This mutation results in a change in the
FT                          corresponding wild type amino acid sequence
FT                          from a Thr residue to Ile residue"
FT   mutation        replace(2110,a)
FT                   /*tag= m
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation      replace(2640,c)
FT                   /*tag= n
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT   AAZ00774" mutation      replace(2826,a)
FT                   /*tag= o
FT                   /note= "This nucleotide differs from the wild type
FT                          sequence in the sequence represented in
FT                          AAZ00774"
XX
PN   WO9937761-A1.
XX
PD   29-JUL-1999.
XX
PF   30-DEC-1998;   98WO-DE03818.
XX
PR   30-DEC-1997;   97DE-1058401.
XX
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI   Hoehe M,  Koepke K,  Timmermann B;
XX
DR   WPI; 1999-479048/40.
XX
PT   Human beta2-adrenergic receptor gene variants, useful for
PT   determining an individuals haplotype
XX
PS   Disclosure; Fig 2a; 27pp; German.
XX
CC   This invention describes novel variant human beta 2-adrenergic receptor
CC   gene sequences which have hypotensive, cardiant, neuroprotective and
CC   immunosuppressive activity. The products of the invention are used in a
CC   method to determine a predisposition for high blood pressure as well as
CC   for abnormal blood pressure and other cardiovascular diseases, including
CC   myocardial infarction and stroke. Other conditions that can be determined
CC   include neuropsychiatric disease, such as depression, anxiety, attention
CC   deficit disorder with hyperactivity, eating disorders, e.g. anorexia
CC   nervosa and bulimia, or post-traumatic stress disorder. Diseases of the
CC   autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and
CC   Riley-Day syndromes having selective noradrenergic-receptor disposition,
CC   or migraine, allergic conditions, e.g. asthma and atopic disorders, and
CC   metabolic illnesses, e.g. morbid obesity including predicting a change in
CC   weight, using body mass index, can also be determined. The beta
CC   2-adrenergic receptor sequence variants can be used to develop
CC   therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor
CC   agonists can be developed. Treatments can be optimized for individuals,
CC   including gene therapy and pharmaceutical intervention therapy. This
CC   sequence represents the wild type human beta 2-adrenergic receptor
CC   gene which is described in the method of the invention.
XX
SQ   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

  Query Match            100.0%;  Score 20;  DB 20;  Length 3451;
  Best Local Similarity  100.0%;  Pred. No. 8.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCCG 20
           ||||||||||||||||||||
Db    1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 10
AAA38339
ID   AAA38339 standard; DNA; 3451 BP.
XX
AC   AAA38339;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human beta-adrenergic receptor-2 gene regulatory region.
XX
KW   Beta-adrenergic receptor-2 gene; regulatory region;
KW   polymorphism; polymorphic marker; cardiovascular disease;
KW   myocardial infarction; unstable angina; hypertension; atherosclerosis;
KW   stroke; prognosis; drug screening; treatment outcome; human; ds.
XX
OS   Homo sapiens.
XX
```

PN WO200022166-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-IB01678.
XX
PR 14-OCT-1998; 98US-0104286.
PR 14-OCT-1998; 98US-0104302.
XX
PA (EURO-) EURONA MEDICAL AB.
XX
PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
XX
DR WPI; 2000-318010/27.
XX
PT Assessing cardiovascular status in humans involves comparing test
PT polymorphic pattern comprising polymorphic positions within genes
PT encoding specific proteins, with reference polymorphic pattern -
XX
PS Disclosure; Page 123-124; 126pp; English.
XX
CC The invention relates to a novel method of assessing the cardiovascular
CC status in an individual and to newly identified polymorphisms in the
CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II
CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
CC aldosterone synthase, endothelin receptor type A and beta-adrenergic
CC receptors 1 and 2. The method comprises determining the sequence at one
CC or more polymorphic positions within these genes, and comparing the
CC pattern of polymorphisms from the individual with a reference polymorphic
CC pattern obtained from a population of individuals exhibiting a
CC predetermined cardiovascular disease status. The polymorphic markers are
CC useful for determining the predisposition of an individual to
CC cardiovascular disorders such as myocardial infarction, unstable angina,
CC hypertension, atherosclerosis and stroke. They are also useful for
CC predicting the likely cardiovascular status of a patient given a
CC treatment regimen comprising administration of cardiovascular drugs
CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
CC blockers) or calcium channel blockers). One or more polymorphic markers
CC provides a basis for predicting the outcome of a treatment regimen.
CC Fragments of the genes comprising a polymorphic site may be used as
CC primers and probes for detecting genetic polymorphisms or in molecular
CC library arrays for high throughput screening. The genes, and the proteins
CC they encode are useful in the screening of potential cardiovascular
CC drugs. Determination of an individual's polymorphic pattern reduces or
CC eliminates trial and error in selecting a treatment for a particular
CC individual cardiovascular patient. It also provides the ability to
CC eliminate patients from clinical trials who are predicted to be
CC non-responsive, or at a risk for an adverse response, to a particular
CC treatment regimen. Adverse results in an early trial can be evaluated to
CC identify polymorphic patterns so that the adverse results can be
CC correlated with a sub-population of the test population, permitting
CC exclusion of such sub-populations from the treatment group. Beneficial
CC drugs can be approved for use in the appropriate population, thereby
CC decreasing the number of patients required for a clinical trial, which in
CC turn decreases the duration and cost of such trials. The present
CC sequence represents the human beta-adrenergic receptor-2 gene
CC regulatory region (GenBank M15169, J02728, M16106). The polymorphic
CC sites identified are 934A/G, 987C/G, 1006A/G, 1120C/G, 1221C/T,
CC 1541C/T and 1568C/T.
XX
SQ Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3451;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCCG 20
||||||||||||||||||||
Db 1523 CCCCGCCGTGGGTCCGCCCG 1542

RESULT 11
AAS18444

ID AAS18444 standard; DNA; 3451 BP.
XX
AC AAS18444;
XX
DT 12-MAR-2002 (first entry)
XX
DE Reference sequence for human beta2AR gene showing polymorphisms.
XX
KW Human; beta2-adrenergic receptor; beta2AR polymorphism; asthma;
KW chromosome 5q31-32; migraine; congestive heart failure; hypertension;
KW ischaemic heart disease; chronic obstructive pulmonary disease; COPD;
KW obesity; diabetes mellitus; premature labour; vasotropic; cardiant;
KW antiarrhythmic; antiasthmatic; antidiabetic; tocolytic; ds.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	variation	replace (565, A)
FT		/*tag= a
FT		/note= "Polymorphic site 1 (PS1)"
FT	variation	replace (879, A)
FT		/*tag= b
FT		/note= "Polymorphic site 2 (PS2)"
FT	variation	replace (934, A)
FT		/*tag= c
FT		/note= "Polymorphic site 3 (PS3)"
FT	variation	replace (1120, C)
FT		/*tag= d
FT		/note= "Polymorphic site 4 (PS4)"
FT	variation	replace (1182, T)
FT		/*tag= e
FT		/note= "Polymorphic site 5 (PS5)"
FT	variation	replace (1221, T)
FT		/*tag= f
FT		/note= "Polymorphic site 6 (PS6)"
FT	variation	replace (1541, T)
FT		/*tag= g
FT		/note= "Polymorphic site 7 (PS7)"
FT	variation	replace (1568, C)
FT		/*tag= h
FT		/note= "Polymorphic site 8 (PS8)"
FT	CDS	1588..2829
FT		/*tag= i
FT		/product= "Beta2AR"
FT	variation	replace (1633, G)
FT		/*tag= j
FT		/note= "Polymorphic site 9 (PS9)"
FT	variation	replace (1666, G)
FT		/*tag= k
FT		/note= "Polymorphic site 10 (PS10)"
FT	variation	replace (1839, A)
FT		/*tag= l
FT		/note= "Polymorphic site 11 (PS11)"
FT	variation	replace (2078, T)
FT		/*tag= m
FT		/note= "Polymorphic site 12 (PS12)"
FT	variation	replace (2110, A)
FT		/*tag= n
FT		/note= "Polymorphic site 13 (PS13)"

XX
PN WO200179252-A1.
XX
PD 25-OCT-2001.
XX
PF 13-APR-2000; 2000WO-US10125.
XX
PR 13-APR-2000; 2000WO-US10125.
XX
PA (GENA-) GENAISSANCE PHARM INC.
PA (UYCI-) UNIV CINCINNATI.
XX
PI Stack CB, Drysdale CM, Stephens JC, Nandabalan K, Judson RS;
PI Liggett SB;

```
XX
DR   WPI; 2002-061968/08.
DR   P-PSDB; AAU10763.
XX
PT   New isolated beta 2-adrenergic receptor polynucleotide, useful for
PT   studying expression and biological function of receptor and for
PT   developing drugs targeting receptor, comprises polymorphism of
PT   adenosine at PS2 and thymine at PS5 -
XX
PS   Claim 1; Fig 1; 67pp; English.
XX
CC   The present invention relates to polymorphisms and haplotypes of
CC   the human beta2-adrenergic receptor (beta2-AR) gene located on
CC   chromosome 5q31-32, and methods for haplotyping and/or genotyping the
CC   beta2AR gene in an individual. The methods of the invention make use of
CC   allele-specific oligonucleotides (ASOs) as probes and primers for
CC   detecting the beta2AR gene polymorphisms. The beta2AR gene polymorphisms
CC   are useful in studying the expression and biological function of beta2AR,
CC   and for developing drugs targeting this receptor. They are also useful
CC   for therapeutic purposes such as treating disorders affected by
CC   expression or function of beta2AR such as congestive heart failure,
CC   arrhythmia, ischaemic heart disease, hypertension, migraine, asthma,
CC   chronic obstructive pulmonary disease (COPD), obesity, diabetes and
CC   premature labour. The method is useful for determining the frequency of
CC   a beta2AR genotype or haplotype in a population. The present sequence
CC   represents a reference sequence for the human beta2AR gene which shows
CC   the polymorphisms in the gene.
XX
SQ   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 24;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCCG 20
           ||||||||||||||||||||
Db    1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 12
AAA46128
ID   AAA46128 standard; DNA; 20 BP.
XX
AC   AAA46128;
XX
DT   05-OCT-2000  (first entry)
XX
DE   Human beta2 adrenergic receptor beta2AR T allele-specific primer #2.
XX
KW   Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW   chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW   congestive heart failure; ischemic heart disease; arrhythmia;
KW   obesity; diabetes; vascular disease; premature labour; migraine;
KW   anaphylaxis; chronic obstructive pulmonary disease;
KW   allele-specific oligonucleotide primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200031307-A1.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US27963.
XX
PR   25-NOV-1998;   98US-0109886.
XX
PA   (UYCI-) UNIV CINCINNATI.
XX
PI   Liggett SB;
XX
DR   WPI; 2000-400107/34.
XX
PT   Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT   receptor (beta 2 AR), useful for predicting genetic disposition to a
PT   disease modified by beta 2 AR expression e.g. congestive heart failure,
PT   hypertension -
XX
PS   Claim 8; Page 11; 56pp; English.
XX
CC   The present sequence is an allele-specific oligonucleotide primer
CC   for the T allele of the human beta2 adrenergic receptor (beta2AR) gene,
CC   which is located on chromosome 5q31 (12). The gene has two different
CC   alleles, and it has been shown that the presence of two copies of the T
CC   allele leads to higher expression of the gene. This is because the
CC   polymorphism is found in the 5' leader sequence, which encodes a peptide
CC   which regulates expression of the beta2AR gene. The polymorphism is
CC   thought to affect individuals' responses to beta-agonists and
CC   beta-antagonists, and is likely to influence their predisposition to
CC   asthma, hypertension, congestive heart failure, ischemic heart disease,
CC   arrhythmia, obesity, diabetes, vascular disease, premature labour,
CC   migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD).
CC   The gene can, therefore, be used to predict the susceptibility of an
CC   individual to these diseases and determine the best treatment.
XX
SQ   Sequence 20 BP; 0 A; 10 C; 7 G; 3 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 21;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 65;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCCG 20
           ||||||||||||||||||| |
Db       1 CCCCGCCGTGGGTCCGCCTG 20


RESULT 13
AAA38785
ID   AAA38785 standard; DNA; 60 BP.
XX
AC   AAA38785;
XX
DT   05-OCT-2000  (first entry)
XX
DE   Human beta2 adrenergic receptor beta2AR gene fragment.
XX
KW   Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
KW   chromosome 5q31(12); disease predisposition; asthma; hypertension;
KW   congestive heart failure; ischemic heart disease; arrhythmia;
KW   obesity; diabetes; vascular disease; premature labour; migraine;
KW   anaphylaxis; chronic obstructive pulmonary disease; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   allele          replace(55,C)
FT                   /*tag=  a
XX
PN   WO200031307-A1.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US27963.
XX
PR   25-NOV-1998;   98US-0109886.
XX
PA   (UYCI-) UNIV CINCINNATI.
XX
PI   Liggett SB;
XX
DR   WPI; 2000-400107/34.
DR   P-PSDB; AAY99531.
XX
PT   Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
PT   receptor (beta 2 AR), useful for predicting genetic disposition to a
PT   disease modified by beta 2 AR expression e.g. congestive heart failure,
PT   hypertension -
```

XX
PS Disclosure; Figure 2; 56pp; English.
XX
CC The present sequence is a fragment of the T allele of the human beta2
CC adrenergic receptor (beta2AR) gene, which is located on chromosome
CC 5q31 (12). The gene has two different alleles, and it has been shown that
CC the presence of two copies of the T allele leads to higher expression of
CC the gene. This is because the polymorphism is found in the 5' leader
CC sequence, which encodes a peptide which regulates expression of the
CC beta2AR gene. The polymorphism is thought to affect individuals'
CC responses to beta-agonists and beta-antagonists, and is likely to
CC influence their predisposition to asthma, hypertension,
CC congestive heart failure, ischemic heart disease, arrhythmia, obesity,
CC diabetes, vascular disease, premature labour, migraine, anaphylaxis and
CC chronic obstructive pulmonary disease (COPD). The gene can, therefore, be
CC used to predict the susceptibility of an individual to these diseases and
CC determine the best treatment.
XX
SQ Sequence 60 BP; 6 A; 24 C; 21 G; 9 T; 0 other;

Query Match 92.0%; Score 18.4; DB 21; Length 60;
Best Local Similarity 95.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCCG 20
||||||||||||||||||| |
Db 37 CCCCGCCGTGGGTCCGCCTG 56

RESULT 14
AAX61116
ID AAX61116 standard; DNA; 2300 BP.
XX
AC AAX61116;
XX
DT 27-JUL-1999 (first entry)
XX
DE Human beta2-adrenergic receptor gene.
XX
KW Alpha1B-adrenergic receptor; human; cardiovascular disease;
KW beta2 adrenergic receptor; genetic variation identification; hypertrophy;
KW disease diagnosis; hypertension; prostatic disease; pulmonary disorder;
KW asthma; peripheral vascular disorder; neuropsychic disorder;
KW endocrine-metabolic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO9924454-A1.
XX
PD 20-MAY-1999.
XX
PF 04-NOV-1998; 98WO-US23496.
XX
PR 10-NOV-1997; 97US-0086232.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Buescher R, Herrmann V, Insel PA;
XX
DR WPI; 1999-327357/27.
XX
PT Pairs of oligonucleotides for amplifying adrenergic receptor genes
XX
PS Disclosure; Fig 2; 58pp; English.
XX
CC This sequence represents the human beta2-adrenergic receptor gene, and
CC is amplified by the primers of the invention. The primers are non-self
CC hybridising; contain at least 15 nucleotides (nt) and has a melting
CC temperature 50-85 deg. C. Each pair of primers is: non-cross-hybridising;
CC anneals to two distinct segments (separated by at least 400 nt); and
CC generates a homogeneous population of gene segments in a polymerase chain
CC reaction (PCR). At least one primer in the pair can extend a 3'-end
CC sequence complementary to a template sequence in a DNA polymerase
CC reaction. The primers are used to amplify segments of the alpha1B and
CC beta2 adrenergic receptor genes, particularly to identify genetic
CC variations for diagnosis of disease. Specifically variations in the
CC alpha1B gene are associated with cardiovascular disease, hypertension and
CC prostatic disease (hypertrophy), and those in the beta2 gene with
CC cardiovascular disease, hypertension and asthma, but variations may also
CC be associated with peripheral vascular, pulmonary, neuropsychic and
CC endocrine-metabolic disorders. These primers allow rapid and specific
CC amplification of large and homogeneous gene segments of the alpha1B and
CC beta2 genes from a complex mixture of DNAs. This makes possible detection
CC of genetic alterations not previously amenable to routine, automated and
CC large-scale sequencing analysis.
XX
SQ Sequence 2300 BP; 495 A; 613 C; 646 G; 546 T; 0 other;

Query Match 92.0%; Score 18.4; DB 20; Length 2300;
Best Local Similarity 95.0%; Pred. No. 40;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCCG 20
||||||||||||||||||| |
Db 729 CCCCGCCGTGGGTCCGCCTG 748

RESULT 15
AAA38340
ID AAA38340 standard; DNA; 2305 BP.
XX
AC AAA38340;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human beta-adrenergic receptor-2 coding region.
XX
KW Beta-adrenergic receptor-2 gene; coding region;
KW polymorphism; polymorphic marker; cardiovascular disease;
KW myocardial infarction; unstable angina; hypertension; atherosclerosis;
KW stroke; prognosis; drug screening; treatment outcome; human; ds.
XX
OS Homo sapiens.
XX
PN WO200022166-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-IB01678.
XX
PR 14-OCT-1998; 98US-0104286.
PR 14-OCT-1998; 98US-0104302.
XX
PA (EURO-) EURONA MEDICAL AB.
XX
PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
XX
DR WPI; 2000-318010/27.
XX
PT Assessing cardiovascular status in humans involves comparing test
PT polymorphic pattern comprising polymorphic positions within genes
PT encoding specific proteins, with reference polymorphic pattern -
XX
PS Disclosure; Page 124-125; 126pp; English.
XX
CC The invention relates to a novel method of assessing the cardiovascular
CC status in an individual and to newly identified polymorphisms in the
CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II
CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
CC aldosterone synthase, endothelin receptor type A and beta-adrenergic
CC receptors 1 and 2. The method comprises determining the sequence at one
CC or more polymorphic positions within these genes, and comparing the
CC pattern of polymorphisms from the individual with a reference polymorphic
CC pattern obtained from a population of individuals exhibiting a
CC predetermined cardiovascular disease status. The polymorphic markers are
CC useful for determining the predisposition of an individual to

CC cardiovascular disorders such as myocardial infarction, unstable angina,
CC hypertension, atherosclerosis and stroke. They are also useful for
CC predicting the likely cardiovascular status of a patient given a
CC treatment regimen comprising administration of cardiovascular drugs
CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
CC blockers) or calcium channel blockers). One or more polymorphic markers
CC provides a basis for predicting the outcome of a treatment regimen.
CC Fragments of the genes comprising a polymorphic site may be used as
CC primers and probes for detecting genetic polymorphisms or in molecular
CC library arrays for high throughput screening. The genes, and the proteins
CC they encode are useful in the screening of potential cardiovascular
CC drugs. Determination of an individual's polymorphic pattern reduces or
CC eliminates trial and error in selecting a treatment for a particular
CC individual cardiovascular patient. It also provides the ability to
CC eliminate patients from clinical trials who are predicted to be
CC non-responsive, or at a risk for an adverse response, to a particular
CC treatment regimen. Adverse results in an early trial can be evaluated to
CC identify polymorphic patterns so that the adverse results can be
CC correlated with a sub-population of the test population, permitting
CC exclusion of such sub-populations from the treatment group. Beneficial
CC drugs can be approved for use in the appropriate population, thereby
CC decreasing the number of patients required for a clinical trial, which in
CC turn decreases the duration and cost of such trials. The present
CC sequence represents the human beta-adrenergic receptor-2 gene
CC coding region (GenBank Y00106/g293708). The polymorphic sites identified
CC are 839A/G, 872C/G, 1045A/G, 1284C/T, 1316A/C, 1846C/G, 2032A/G,
CC 2068 no insert/G/C and 2070 no insert/C.
XX
SQ Sequence 2305 BP; 495 A; 616 C; 649 G; 545 T; 0 other;

Query Match 92.0%; Score 18.4; DB 21; Length 2305;
Best Local Similarity 95.0%; Pred. No. 40;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCGCCGTGGGTCCGCCCG 20
||||||||||||||||||| |
Db 729 CCCCGCCGTGGGTCCGCCTG 748

Search completed: November 2, 2002, 16:13:15
Job time : 85.7273 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 13:22:40 ; Search time 387.636 Seconds
(without alignments)
1079.699 Million cell updates/sec

Title: US-09-856-803-8
Perfect score: 20
Sequence: 1 ccccgccgtgggtccgcctg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	20	100.0	2063	9	BC012481	BC012481 Homo sapi
2	20	100.0	2305	9	HSBAR	Y00106 Human gene
3	20	100.0	3451	6	AX022517	AX022517 Sequence
4	20	100.0	3451	6	AX022518	AX022518 Sequence
5	20	100.0	3451	6	AX022520	AX022520 Sequence
6	20	100.0	3451	6	AX022521	AX022521 Sequence
7	20	100.0	3451	6	AX022523	AX022523 Sequence
8	20	100.0	3458	9	HUMADRBRA	J02960 Human beta-
9	18.4	92.0	51	6	AX204248	AX204248 Sequence
10	18.4	92.0	230	6	AR164456	AR164456 Sequence
11	18.4	92.0	1970	9	HSBARR	X04827 Human mRNA
12	18.4	92.0	3451	6	AX022519	AX022519 Sequence
13	18.4	92.0	3451	6	AX022522	AX022522 Sequence
14	18.4	92.0	3451	6	AX332732	AX332732 Sequence
15	18.4	92.0	3451	6	AX334116	AX334116 Sequence
16	18.4	92.0	3451	9	HUMADRBR	M15169 Human beta-
17	18.4	92.0	133042	9	AC011354	AC011354 Homo sapi
18	18.4	92.0	134413	9	AC011334	AC011334 Homo sapi
c 19	17.4	87.0	1770	6	AX077832	AX077832 Sequence
c 20	17.4	87.0	1770	6	E52155	E52155 Gene encodi
c 21	17.4	87.0	1770	8	AB045592	AB045592 Perilla f
22	17	85.0	57108	2	AC099942	AC099942 Mus muscu
c 23	17	85.0	178000	1	SCO590463	AL590463 Streptomy
24	17	85.0	178073	1	SCO590464	AL590464 Streptomy
c 25	16.8	84.0	549	8	AF177153	AF177153 Cateracti
c 26	16.8	84.0	717	9	HSA332430	AJ332430 Homo sapi
c 27	16.8	84.0	2057	3	AY060726	AY060726 Drosophil
28	16.8	84.0	10789	2	AC017895	AC017895 Drosophil
29	16.8	84.0	23536	1	AE008708	AE008708 Salmonell
30	16.8	84.0	37866	1	SEN320483	AJ320483 Salmonell
c 31	16.8	84.0	39972	2	AC087250	AC087250 Homo sapi
32	16.8	84.0	85928	2	AC094287	AC094287 Rattus no
33	16.8	84.0	99281	2	AC110492	AC110492 Homo sapi
c 34	16.8	84.0	119703	2	AC103510	AC103510 Rattus no
35	16.8	84.0	128804	2	AC099273	AC099273 Rattus no
36	16.8	84.0	134507	2	AC103158	AC103158 Rattus no
37	16.8	84.0	142519	9	HS620E11	AL031667 Human DNA
38	16.8	84.0	154542	2	AC079040	AC079040 Mus muscu
c 39	16.8	84.0	175691	2	AC007615	AC007615 Homo sapi
40	16.8	84.0	183478	2	AC105517	AC105517 Rattus no
41	16.8	84.0	188873	3	AC099009	AC099009 Drosophil
42	16.8	84.0	191496	2	AC009130	AC009130 Homo sapi
c 43	16.8	84.0	191601	2	AC092143	AC092143 Homo sapi
44	16.8	84.0	196337	3	AC005894	AC005894 Drosophil
c 45	16.8	84.0	208008	2	AC009093	AC009093 Homo sapi

ALIGNMENTS

RESULT 1
BC012481
LOCUS BC012481 2063 bp mRNA linear PRI 20-AUG-2001
DEFINITION Homo sapiens, Similar to adrenergic, beta-2-, receptor, surface, clone MGC:21367 IMAGE:4538187, mRNA, complete cds.
ACCESSION BC012481
VERSION BC012481.1 GI:15214693
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2063)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP

```
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: villalon@bcm.tmc.edu.
            Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
            A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
            Muzny,D.M., Gibbs,R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 28 Row: k Column: 6
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 178203.
FEATURES              Location/Qualifiers
     source           1. .2063
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="MGC:21367 IMAGE:4538187"
                      /tissue_type="Prostate, adenocarcinoma."
                      /clone_lib="NIH_MGC_91"
                      /lab_host="DH10B"
                      /note="Vector: pCMV-SPORT6"
     CDS              222. .1463
                      /codon_start=1
                      /product="Similar to adrenergic, beta-2-, receptor,
                      surface"
                      /protein_id="AAH12481.1"
                      /db_xref="GI:15214694"
                      /translation="MGQPGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
                      LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
                      NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                      SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                      YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                      IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                      AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                      TVPSDNIDSPGRNCSTNDSLL"
BASE COUNT      512 a    522 c    498 g    531 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 9;  Length 2063;
  Best Local Similarity  100.0%;  Pred. No. 68;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||||||||
Db    157 CCCCGCCGTGGGTCCGCCTG 176


RESULT 2
HSBAR
LOCUS       HSBAR                   2305 bp    DNA     linear   PRI 12-SEP-1993
DEFINITION  Human gene for beta-adrenergic receptor (beta-2 subtype).
ACCESSION   Y00106
VERSION     Y00106.1  GI:29370
KEYWORDS    beta-adrenergic receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2305)
  AUTHORS   Schofield,P.R., Rhee,L.M. and Peralta,E.G.
  TITLE     Primary structure of the human beta-adrenergic receptor gene
  JOURNAL   Nucleic Acids Res. 15 (8), 3636 (1987)
  MEDLINE   87203400
REFERENCE   2  (bases 1 to 2305)
  AUTHORS   Schofield,P.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-OCT-1987)
FEATURES              Location/Qualifiers
     source           1. .2305
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="lambdahbetaAR17"
                      /clone_lib="Maniatis human"
     CDS              794. .2035
                      /note="beta-adrenergic receptor (AA 1 - 413)"
                      /codon_start=1
                      /protein_id="CAA68289.1"
                      /db_xref="GI:29371"
                      /db_xref="SWISS-PROT:P07550"
                      /translation="MGQPGNGSAFLLAPNRSHAPDHDVTQQRDEVWVVGMGIVMSLIV
                      LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
                      NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                      SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                      YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                      IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                      AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                      TVPSDNIDSQGRNCSTNDSLL"
     misc_feature     809. .817
                      /note="N-linked glycosylation site"
     misc_feature     836. .844
                      /note="N-linked glycosylation site"
     misc_feature     896. .967
                      /note="membrane spanning domain I"
     misc_feature     1007. .1078
                      /note="membrane spanning domain II"
     misc_feature     1114. .1180
                      /note="membrane spanning domain III"
     misc_feature     1247. .1315
                      /note="membrane spanning domain IV"
     misc_feature     1385. .1450
                      /note="membrane spanning domain V"
     misc_feature     1616. .1687
                      /note="membrane spanning domain VI"
     misc_feature     1712. .1774
                      /note="membrane spanning domain VII"
BASE COUNT      495 a    616 c    649 g    545 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 9;  Length 2305;
  Best Local Similarity  100.0%;  Pred. No. 66;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||||||||
Db    729 CCCCGCCGTGGGTCCGCCTG 748


RESULT 3
AX022517
LOCUS       AX022517                3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9937761.
ACCESSION   AX022517
VERSION     AX022517.1  GI:10046115
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 1 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES              Location/Qualifiers
     source           1. .3451
                      /organism="unidentified"
                      /db_xref="taxon:32644"
BASE COUNT      794 a    871 c    892 g    894 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 3451;
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  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           ||||||||||||||||||||
Db    1523 CCCCGCCGTGGGTCCGCCTG 1542


RESULT 4
AX022518
LOCUS       AX022518               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9937761.
ACCESSION   AX022518
VERSION     AX022518.1  GI:10046116
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 2 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      790 a    872 c    895 g    894 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           ||||||||||||||||||||
Db    1523 CCCCGCCGTGGGTCCGCCTG 1542


RESULT 5
AX022520
LOCUS       AX022520               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from Patent WO9937761.
ACCESSION   AX022520
VERSION     AX022520.1  GI:10046119
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 4 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      789 a    872 c    896 g    894 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           ||||||||||||||||||||
Db    1523 CCCCGCCGTGGGTCCGCCTG 1542


RESULT 6
AX022521
LOCUS       AX022521               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 5 from Patent WO9937761.
ACCESSION   AX022521
VERSION     AX022521.1  GI:10046120
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 5 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      790 a    872 c    895 g    894 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           ||||||||||||||||||||
Db    1523 CCCCGCCGTGGGTCCGCCTG 1542


RESULT 7
AX022523
LOCUS       AX022523               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 7 from Patent WO9937761.
ACCESSION   AX022523
VERSION     AX022523.1  GI:10046122
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 7 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      789 a    872 c    896 g    894 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 3451;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           ||||||||||||||||||||
Db    1523 CCCCGCCGTGGGTCCGCCTG 1542


RESULT 8
HUMADRBRA
LOCUS       HUMADRBRA              3458 bp    DNA     linear   PRI 13-FEB-1996
DEFINITION  Human beta-2-adrenergic receptor gene, complete cds.
ACCESSION   J02960
VERSION     J02960.1  GI:178203
```

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KEYWORDS    adrenergic receptor; beta-2 adrenergic receptor.
SOURCE      Homo sapiens (clone: H-beta-R-[9,10,11].) epidermis DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3458)
  AUTHORS   Emorine,L.J., Marullo,S., Delavier-Klutchko,C., Kaveri,S.V.,
            Durieu-Trautmann,O. and Strosberg,A.D.
  TITLE     Structure of the gene for human beta 2-adrenergic receptor:
            expression and promoter characterization
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (20), 6995-6999 (1987)
  MEDLINE   88041037
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by L.J.Emorine, 25-AUG-1987.
FEATURES             Location/Qualifiers
     source          1. .3458
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="5q31-q32"
                     /clone="H-beta-R-[9,10,11]."
                     /cell_line="A431"
                     /tissue_type="epidermis"
     CDS             277. .1032
                     /note="ORF; putative"
                     /codon_start=1
                     /product="unknown protein"
                     /protein_id="AAA88016.1"
                     /db_xref="GI:560762"
                     /translation="MFEREYTGLPGVCWEGSIISARVRQVRSTQMETSVSVSLWMPPS
                     QRVFTFCVCHHVFVLLGASVFVSGRVSVLDRGDFVPDGFCVRARASVHVGELGGCVSV
                     SMAVVRYKSEHVCQGVFVPVCACLGGHSRFLPNVGQCRCAALCLETSSRAGAQGRQVA
                     ATEEPKAPGLAGKHTTSSFSPLGPARVAGKQWWPALQGAVGPRPGQPQEKEGEGRGGK
                     GEECLAPSRLPACHWPKVPVRHGEGSSPKVLCT"
     mRNA            1045. .3057
                     /note="beta-2-adrenergic receptor mRNA (alt.)"
     mRNA            1055. .3057
                     /note="beta-2-adrenergic receptor mRNA (alt.)"
     mRNA            1064. .3057
                     /note="beta-2-adrenergic receptor mRNA (alt.)"
     gene            1264. .2505
                     /gene="ADRB2"
     CDS             1264. .2505
                     /gene="ADRB2"
                     /codon_start=1
                     /product="beta-2 adrenergic receptor"
                     /protein_id="AAA88017.1"
                     /db_xref="GI:178204"
                     /db_xref="GDB:G00-120-541"
                     /translation="MGQPGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
                     LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
                     NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                     IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                     AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEI .PGTEDPVGHQG
                     TVPSDNIDSQGRNCSTNDSLL"
BASE COUNT      777 a    890 c    886 g    905 t
ORIGIN      1 bp upstream of EcoRI site; chromosome 5q31-q32.

  Query Match             100.0%;  Score 20;  DB 9;  Length 3458;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          ||||||||||||||||||||
Db   1199 CCCCGCCGTGGGTCCGCCTG 1218


RESULT 9
AX204248
LOCUS       AX204248                 51 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 354 from Patent WO0148245.
ACCESSION   AX204248
VERSION     AX204248.1  GI:15393760
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0148245-A 354 05-JUL-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     variation       26
                     /note="single nucleotide polymorphism
                     Accession number cg43040273"
BASE COUNT        5 a      24 c      18 g       4 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 51;
  Best Local Similarity   95.0%;  Pred. No. 7.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          |||||||||||||||||| |
Db      8 CCCCGCCGTGGGTCCGCCCG 27


RESULT 10
AR164456
LOCUS       AR164456                 230 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 8 from patent US 6273893.
ACCESSION   AR164456
VERSION     AR164456.1  GI:16237489
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 230)
  AUTHORS   McAllen,J. III, Overaker,D.W. and Cooper,K.L.
  TITLE     Absorbable rivet/pin applier for use in surgical procedures
  JOURNAL   Patent: US 6273893-A 8 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .230
                     /organism="unknown"
BASE COUNT       42 a      91 c      70 g      27 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 230;
  Best Local Similarity   95.0%;  Pred. No. 5.6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          |||||||||||||||||| |
Db    155 CCCCGCCGTGGGTCCGCCCG 174


RESULT 11
HSBARR
LOCUS       HSBARR                  1970 bp    mRNA    linear   PRI 12-SEP-1993
DEFINITION  Human mRNA for brain beta-adrenergic receptor.
ACCESSION   X04827
VERSION     X04827.1  GI:29372
KEYWORDS    beta-adrenergic receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1970)
  AUTHORS   Chung,F.Z., Lentes,K.U., Gocayne,J., Fitzgerald,M., Robinson,D.,
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            Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
  TITLE     Cloning and sequence analysis of the human brain beta-adrenergic
            receptor. Evolutionary relationship to rodent and avian
            beta-receptors and porcine muscarinic receptors
  JOURNAL   FEBS Lett. 211 (2), 200-206 (1987)
  MEDLINE   87105974
REFERENCE   2  (bases 1 to 1970)
  AUTHORS   Kerlavage,A.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-SEP-1987)
COMMENT     substantial corrections are reported in [2]
            Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
FEATURES             Location/Qualifiers
     source          1. .1970
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="neonatal human brain stem"
     CDS             178. .1419
                     /note="beta-adrenergic receptor (AA 1-413)"
                     /codon_start=1
                     /protein_id="CAA28511.1"
                     /db_xref="GI:29373"
                     /db_xref="SWISS-PROT:P07550"
                     /translation="MGQPGNGSAFLLAPNGSHAPDHDVTQERDEVWVVGMGIVMSLIV
                     LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
                     NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                     IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                     AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                     TVPSDNIDSQGRNCSTNDSLL"
     misc_feature    794. .799
                     /note="pot. glucocorticoid-responsive element"
     misc_feature    965. .970
                     /note="pot. glucocorticoid-responsive element"
     misc_feature    1459. .1464
                     /note="pot. glucocorticoid-responsive element"
     misc_feature    1491. .1496
                     /note="pot. polyA signal"
     misc_feature    1502. .1507
                     /note="pot. polyA signal"
     misc_feature    1952. .1957
                     /note="pot. polyA signal"
     polyA_site      1970
                     /note="polyA site"
BASE COUNT      459 a    508 c    482 g    521 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 9;  Length 1970;
  Best Local Similarity   95.0%;  Pred. No. 3.5e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||||||||||||||| |
Db     113 CCCCGCCGTGGGTCCGCCCG 132


RESULT 12
AX022519
LOCUS       AX022519               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 3 from Patent WO9937761.
ACCESSION   AX022519
VERSION     AX022519.1  GI:10046118
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 3 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      789 a    872 c    897 g    893 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 3451;
  Best Local Similarity   95.0%;  Pred. No. 3.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||||||||||||||| |
Db    1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 13
AX022522
LOCUS       AX022522               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 6 from Patent WO9937761.
ACCESSION   AX022522
VERSION     AX022522.1  GI:10046121
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 6 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      789 a    873 c    897 g    892 t
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 3451;
  Best Local Similarity   95.0%;  Pred. No. 3.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCCCGCCGTGGGTCCGCCTG 20
           |||||||||||||||||| |
Db    1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 14
AX332732
LOCUS       AX332732               3451 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 3241 from Patent WO0194629.
ACCESSION   AX332732
VERSION     AX332732.1  GI:18123366
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 3241 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      790 a    873 c    895 g    893 t
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ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 6;  Length 3451;
  Best Local Similarity  95.0%;  Pred. No. 3.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
          |||||||||||||||||| |
Db   1523 CCCCGCCGTGGGTCCGCCCG 1542


RESULT 15
AX334116
LOCUS       AX334116               3451 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 4625 from Patent WO0194629.
ACCESSION   AX334116
VERSION     AX334116.1  GI:18124835
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 4625 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .3451
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      790 a    873 c    895 g    893 t
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 6;  Length 3451;
  Best Local Similarity  95.0%;  Pred. No. 3.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCCCGCCGTGGGTCCGCCTG 20
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Db   1523 CCCCGCCGTGGGTCCGCCCG 1542


Search completed: November  2, 2002, 16:50:27
Job time : 390.636 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 13:22:40 ; Search time 290.727 Seconds
(without alignments)
1079.699 Million cell updates/sec

Title: US-09-856-803-6
Perfect score: 15
Sequence: 1 gtccgcctgctgagg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
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7: gb_ph:*
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14: gb_vi:*
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16: em_fun:*
17: em_hum:*
18: em_in:*
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21: em_or:*
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28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		15	100.0	2063	9	BC012481	BC012481 Homo sapi
2		15	100.0	2305	9	HSBAR	Y00106 Human gene
3		15	100.0	3451	6	AX022517	AX022517 Sequence
4		15	100.0	3451	6	AX022518	AX022518 Sequence
5		15	100.0	3451	6	AX022520	AX022520 Sequence
6		15	100.0	3451	6	AX022521	AX022521 Sequence
7		15	100.0	3451	6	AX022523	AX022523 Sequence
8		15	100.0	3458	9	HUMADRBRA	J02960 Human beta-
9	c	15	100.0	31740	2	AC025128	AC025128 Homo sapi
10	c	15	100.0	158755	2	AC091404	AC091404 Sus scrof
11		15	100.0	170559	2	AC095307	AC095307 Rattus no
12	c	14	93.3	706	5	AB025351	AB025351 Rana cate
13		14	93.3	1100	6	A22950	A22950 H.sapiens m
14		14	93.3	1100	6	AR150761	AR150761 Sequence
15		14	93.3	2470	6	I12881	I12881 Sequence 14
16	c	14	93.3	2509	9	AK055768	AK055768 Homo sapi
17	c	14	93.3	2925	4	AB020986	AB020986 Canis fam
18	c	14	93.3	2925	6	E59801	E59801 Canine obsi
19	c	14	93.3	3113	10	RNU10900	U10900 Rattus norv
20		14	93.3	5467	6	I12880	I12880 Sequence 12
21		14	93.3	6232	6	A22938	A22938 H.sapiens m
22		14	93.3	6232	6	AR150755	AR150755 Sequence
23		14	93.3	7175	6	AR022380	AR022380 Sequence
24		14	93.3	7175	6	AR063883	AR063883 Sequence
25		14	93.3	7175	6	AR067883	AR067883 Sequence
26		14	93.3	7175	6	AR105184	AR105184 Sequence
27		14	93.3	7177	9	HUMCACHNTA	M94173 Human N-typ
28	c	14	93.3	7253	1	SMASHLAB	M22618 Serratia ma
29		14	93.3	7266	6	AR118079	AR118079 Sequence
30		14	93.3	7362	6	AR022379	AR022379 Sequence
31		14	93.3	7362	6	AR063882	AR063882 Sequence
32		14	93.3	7362	6	AR067882	AR067882 Sequence
33		14	93.3	7362	6	AR105183	AR105183 Sequence
34		14	93.3	7364	6	AX333697	AX333697 Sequence
35		14	93.3	7364	9	HUMCACHNT	M94172 Human N-typ
36		14	93.3	10627	6	I13706	I13706 Sequence 12
37		14	93.3	12222	9	HUMA1ATP	K02212 Human alpha
38	c	14	93.3	25360	2	AC017698	AC017698 Drosophil
39	c	14	93.3	32539	9	HSL1C2	Z49154 Human DNA f
40	c	14	93.3	64632	2	AC013655	AC013655 *Homo sapi*
41		14	93.3	80069	2	AC019671	AC019671 Drosophil
42		14	93.3	88941	2	AC095779	AC095779 Rattus no
43		14	93.3	110000	2	LMFLCHR26_1	Continuation (2 of
44	c	14	93.3	145550	2	AP001900	AP001900 Homo sapi
45		14	93.3	147505	9	CNS01DTA	AL132708 Human chr

ALIGNMENTS

RESULT 1
BC012481
LOCUS BC012481 2063 bp mRNA linear PRI 20-AUG-2001
DEFINITION Homo sapiens, Similar to adrenergic, beta-2-, receptor, surface, clone MGC:21367 IMAGE:4538187, mRNA, complete cds.
ACCESSION BC012481
VERSION BC012481.1 GI:15214693
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2063)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP

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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: villalon@bcm.tmc.edu.
            Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
            A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
            Muzny,D.M., Gibbs,R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 28 Row: k Column: 6
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 178203.
FEATURES             Location/Qualifiers
     source          1. .2063
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="MGC:21367 IMAGE:4538187"
                     /tissue_type="Prostate, adenocarcinoma."
                     /clone_lib="NIH_MGC_91"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             222. .1463
                     /codon_start=1
                     /product="Similar to adrenergic, beta-2-, receptor,
                     surface"
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                     /db_xref="GI:15214694"
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                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                     IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
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BASE COUNT      512 a    522 c    498 g    531 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 7.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCTGCTGAGG 15
          |||||||||||||||
Db    168 GTCCGCCTGCTGAGG 182


RESULT 2
HSBAR
LOCUS       HSBAR                   2305 bp    DNA     linear   PRI 12-SEP-1993
DEFINITION  Human gene for beta-adrenergic receptor (beta-2 subtype).
ACCESSION   Y00106
VERSION     Y00106.1  GI:29370
KEYWORDS    beta-adrenergic receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2305)
  AUTHORS   Schofield,P.R., Rhee,L.M. and Peralta,E.G.
  TITLE     Primary structure of the human beta-adrenergic receptor gene
  JOURNAL   Nucleic Acids Res. 15 (8), 3636 (1987)
  MEDLINE   87203400
REFERENCE   2  (bases 1 to 2305)
  AUTHORS   Schofield,P.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-OCT-1987)
FEATURES             Location/Qualifiers
     source          1. .2305
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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     CDS             794. .2035
                     /note="beta-adrenergic receptor (AA 1 - 413)"
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                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
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ORIGIN

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCTGCTGAGG 15
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Db    740 GTCCGCCTGCTGAGG 754


RESULT 3
AX022517
LOCUS       AX022517                3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9937761.
ACCESSION   AX022517
VERSION     AX022517.1  GI:10046115
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 1 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .3451
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                     /db_xref="taxon:32644"
BASE COUNT      794 a    871 c    892 g    894 t
ORIGIN

  Query Match           100.0%;  Score 15;  DB 6;  Length 3451;
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  Best Local Similarity   100.0%;  Pred. No. 6.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCTGCTGAGG 15
          |||||||||||||||
Db   1534 GTCCGCCTGCTGAGG 1548


RESULT 4
AX022518
LOCUS       AX022518               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9937761.
ACCESSION   AX022518
VERSION     AX022518.1  GI:10046116
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 2 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      790 a    872 c    895 g    894 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 6.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCTGCTGAGG 15
          |||||||||||||||
Db   1534 GTCCGCCTGCTGAGG 1548


RESULT 5
AX022520
LOCUS       AX022520               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from Patent WO9937761.
ACCESSION   AX022520
VERSION     AX022520.1  GI:10046119
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 4 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      789 a    872 c    896 g    894 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 6.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCTGCTGAGG 15
          |||||||||||||||
Db   1534 GTCCGCCTGCTGAGG 1548


RESULT 6
AX022521
LOCUS       AX022521               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 5 from Patent WO9937761.
ACCESSION   AX022521
VERSION     AX022521.1  GI:10046120
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 5 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
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BASE COUNT      790 a    872 c    895 g    894 t
ORIGIN

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Qy      1 GTCCGCCTGCTGAGG 15
          |||||||||||||||
Db   1534 GTCCGCCTGCTGAGG 1548


RESULT 7
AX022523
LOCUS       AX022523               3451 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 7 from Patent WO9937761.
ACCESSION   AX022523
VERSION     AX022523.1  GI:10046122
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3451)
  AUTHORS   Hoehe,M., Koepke,K. and Timmermann,B.
  TITLE     Novel sequence variants of the human beta2-adrenergic receptor gene
            and use thereof
  JOURNAL   Patent: WO 9937761-A 7 29-JUL-1999;
            HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
            MOLEKULA (DE); TIMMERMANN BERND (DE)
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
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BASE COUNT      789 a    872 c    896 g    894 t
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  Best Local Similarity   100.0%;  Pred. No. 6.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCGCCTGCTGAGG 15
          |||||||||||||||
Db   1534 GTCCGCCTGCTGAGG 1548


RESULT 8
HUMADRBRA
LOCUS       HUMADRBRA              3458 bp    DNA     linear   PRI 13-FEB-1996
DEFINITION  Human beta-2-adrenergic receptor gene, complete cds.
ACCESSION   J02960
VERSION     J02960.1  GI:178203
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KEYWORDS    adrenergic receptor; beta-2 adrenergic receptor.
SOURCE      Homo sapiens (clone: H-beta-R-[9,10,11].) epidermis DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3458)
  AUTHORS   Emorine,L.J., Marullo,S., Delavier-Klutchko,C., Kaveri,S.V.,
            Durieu-Trautmann,O. and Strosberg,A.D.
  TITLE     Structure of the gene for human beta 2-adrenergic receptor:
            expression and promoter characterization
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (20), 6995-6999 (1987)
  MEDLINE   88041037
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by L.J.Emorine, 25-AUG-1987.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="5q31-q32"
                     /clone="H-beta-R-[9,10,11]."
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                     /tissue_type="epidermis"
     CDS             277. .1032
                     /note="ORF; putative"
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                     /product="unknown protein"
                     /protein_id="AAA88016.1"
                     /db_xref="GI:560762"
                     /translation="MFEREYTGLPGVCWEGSIISARVRQVRSTQMETSVSVSLWMPPS
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     mRNA            1045. .3057
                     /note="beta-2-adrenergic receptor mRNA (alt.)"
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                     /note="beta-2-adrenergic receptor mRNA (alt.)"
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                     /note="beta-2-adrenergic receptor mRNA (alt.)"
     gene            1264. .2505
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                     /product="beta-2 adrenergic receptor"
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                     /db_xref="GI:178204"
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                     SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                     YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
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                     TVPSDNIDSQGRNCSTNDSLL"
BASE COUNT      777 a    890 c    886 g    905 t
ORIGIN      1 bp upstream of EcoRI site; chromosome 5q31-q32.

  Query Match             100.0%;  Score 15;  DB 9;  Length 3458;
  Best Local Similarity   100.0%;  Pred. No. 6.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCTGCTGAGG 15
           |||||||||||||||
Db    1210 GTCCGCCTGCTGAGG 1224


RESULT 9
AC025128/c
LOCUS       AC025128               31740 bp    DNA     linear   HTG 13-JUL-2000
DEFINITION  Homo sapiens clone RP11-307E16, LOW-PASS SEQUENCE SAMPLING.
ACCESSION   AC025128
VERSION     AC025128.1  GI:7158939
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 31740)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens, clone RP11-307E16
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 31740)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
            Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
            Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
            Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
            Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
            Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
            McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
            Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
            Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
            Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
            Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L7794
                Center clone name: 307_E_16
            --------------.
            * NOTE: This record contains 36 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            *       1     799: contig of 799 bp in length
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            *     900    1693: contig of 794 bp in length
            *    1694 1793: gap of     100 bp
            *    1794    2579: contig of 786 bp in length
            *    2580 2679: gap of     100 bp
            *    2680    3436: contig of 757 bp in length
            *    3437 3536: gap of     100 bp
            *    3537    4294: contig of 758 bp in length
            *    4295 4394: gap of     100 bp
            *    4395    5145: contig of 751 bp in length
            *    5146 5245: gap of     100 bp
            *    5246    6045: contig of 800 bp in length
            *    6046 6145: gap of     100 bp
            *    6146    6962: contig of 817 bp in length
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            *     6963 7062: gap of      100 bp
            *     7063    7843: contig of 781 bp in length
            *     7844 7943: gap of      100 bp
            *     7944    8728: contig of 785 bp in length
            *     8729 8828: gap of      100 bp
            *     8829    9582: contig of 754 bp in length
            *     9583 9682: gap of      100 bp
            *     9683   10452: contig of 770 bp in length
            *    10453 10552: gap of      100 bp
            *    10553   11353: contig of 801 bp in length
            *    11354 11453: gap of      100 bp
            *    11454   12246: contig of 793 bp in length
            *    12247 12346: gap of      100 bp
            *    12347   13148: contig of 802 bp in length
            *    13149 13248: gap of      100 bp
            *    13249   14028: contig of 780 bp in length
            *    14029 14128: gap of      100 bp
            *    14129   14900: contig of 772 bp in length
            *    14901 15000: gap of      100 bp
            *    15001   15794: contig of 794 bp in length
            *    15795 15894: gap of      100 bp
            *    15895   16701: contig of 807 bp in length
            *    16702 16801: gap of      100 bp
            *    16802   17587: contig of 786 bp in length
            *    17588 17687: gap of      100 bp
            *    17688   18473: contig of 786 bp in length
            *    18474 18573: gap of      100 bp
            *    18574   19354: contig of 781 bp in length
            *    19355 19454: gap of      100 bp
            *    19455   20237: contig of 783 bp in length
            *    20238 20337: gap of      100 bp
            *    20338   21119: contig of 782 bp in length
            *    21120 21219: gap of      100 bp
            *    21220   21995: contig of 776 bp in length
            *    21996 22095: gap of      100 bp
            *    22096   22872: contig of 777 bp in length
            *    22873 22972: gap of      100 bp
            *    22973   23749: contig of 777 bp in length
            *    23750 23849: gap of      100 bp
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            *    24644 24743: gap of      100 bp
            *    24744   25561: contig of 818 bp in length
            *    25562 25661: gap of      100 bp
            *    25662   26424: contig of 763 bp in length
            *    26425 26524: gap of      100 bp
            *    26525   27317: contig of 793 bp in length
            *    27318 27417: gap of      100 bp
            *    27418   28208: contig of 791 bp in length
            *    28209 28308: gap of      100 bp
            *    28309   29105: contig of 797 bp in length
            *    29106 29205: gap of      100 bp
            *    29206   29995: contig of 790 bp in length
            *    29996 30095: gap of      100 bp
            *    30096   30893: contig of 798 bp in length
            *    30894 30993: gap of      100 bp
            *    30994   31740: contig of 747 bp in length.
FEATURES             Location/Qualifiers
     source          1. .31740
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="RP11-307E16"
                     /clone_lib="RPCI-11 Human Male BAC"
BASE COUNT     7151 a   7154 c   6162 g   7609 t   3664 others
ORIGIN

  Query Match           100.0%;  Score 15;  DB 2;  Length 31740;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCTGCTGAGG 15
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Db    8257 GTCCGCCTGCTGAGG 8243
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RESULT 10
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LOCUS       AC091404              158755 bp    DNA     linear   HTG 19-APR-2001
DEFINITION  Sus scrofa clone RP44-74O11, WORKING DRAFT SEQUENCE, 6 unordered
            pieces.
ACCESSION   AC091404
VERSION     AC091404.1  GI:13677075
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 158755)
  AUTHORS   Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
            Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S.,
            Guan,X., Gupta,J., Ho,S.-L., Idol,J.R., Karlins,E., Lee-Lin,S.-Q.,
            Legaspi,R., Lim,M., Maduro,Q.L., Maduro,V.B., Masiello,C.,
            Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A.,
            Shevchenko,Y., Snyder,B., Stantripop,S., Thomas,J.W., Thomas,P.J.,
            Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
            Wetherby,K.D., Zhang,L.-H. and Green,E.D.
  TITLE     NISC Comparative Sequencing Initiative
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 158755)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2001) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT     -------------- Genome Center
                 Center: NIH Intramural Sequencing Center
                 Center code: NISC
                 Web site: http://www.nisc.nih.gov
                 Contact: nisc_mouse@nhgri.nih.gov
            -------------- Project Information
                 Center project name: akp
                 Center clone name: 074O11
            -------------- Summary Statistics
                 Sequencing vector: plasmid; n/a; 100% of reads
                 Chemistry: Dye-terminator Big Dye; 100% of reads
                 Assembly program: Phrap; version 0.990319
                 Consensus quality: 155345 bases at least Q40
                 Consensus quality: 156172 bases at least Q30
                 Consensus quality: 156597 bases at least Q20
                 Insert size: 154000; agarose-fp
                 Insert size: 189000; pulse-field-gel
                 Insert size: 158255; sum-of-contigs
                 Quality coverage: 10.68x in Q20 bases; agarose-fp
                 Quality coverage: 8.70x in Q20 bases; pulse-field-gel
                 Quality coverage: 10.39x in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     3649: contig of 3649 bp in length
            *     3650     3749: gap of unknown length
            *     3750    13662: contig of 9913 bp in length
            *    13663    13762: gap of unknown length
            *    13763    32623: contig of 18861 bp in length
            *    32624    32723: gap of unknown length
            *    32724    55171: contig of 22448 bp in length
            *    55172    55271: gap of unknown length
            *    55272    86367: contig of 31096 bp in length
            *    86368    86467: gap of unknown length
            *    86468   158755: contig of 72288 bp in length.
FEATURES             Location/Qualifiers
     source          1. .158755
                     /organism="Sus scrofa"
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                     /clone="RP44-74O11"
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                     vector_side:left"
     misc_feature    3750. .13662
                     /note="assembly_fragment"
     misc_feature    13763. .32623
                     /note="assembly_fragment"
     misc_feature    32724. .55171
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:left"
     misc_feature    55272. .86367
                     /note="assembly_fragment"
     misc_feature    86468. .158755
                     /note="assembly_fragment"
BASE COUNT    41826 a  38951 c  37930 g  39519 t    529 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 2;  Length 158755;
  Best Local Similarity   100.0%;  Pred. No. 5.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCTGCTGAGG 15
           |||||||||||||||
Db   89572 GTCCGCCTGCTGAGG 89558


RESULT 11
AC095307
LOCUS       AC095307              170559 bp    DNA     linear   HTG 20-DEC-2001
DEFINITION  Rattus norvegicus clone CH230-23A17, *** SEQUENCING IN PROGRESS
            ***, 60 unordered pieces.
ACCESSION   AC095307
VERSION     AC095307.2  GI:17943698
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 170559)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
            Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
            Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
            Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
            Carte ,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
            Chen,S., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
            Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
            Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
            Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
            Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
            Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
            Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
            Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
            Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
            Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
            Hollins,B,, Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
            Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
            Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
            Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
            Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
            Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
            Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
            Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
            Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
            Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N.,
            Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
            Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
            Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
            Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
            Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
            Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
            Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
            Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N.,
            Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
            Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
            Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
            Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 170559)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-SEP-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Dec 20, 2001 this sequence version replaced gi:15625861.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GEGH
                Center clone name: CH230-23A17
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329First call to
            findPhrapList
                Consensus quality: 144777 bases at least Q40
                Consensus quality: 151419 bases at least Q30
                Consensus quality: 157099 bases at least Q20
                Estimated insert size: 145164; sum-of-contigs estimation
                Quality coverage: 0x in Q20 bases; agarose-fp estimation
                Quality coverage: 2.5x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 60 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *    10093    16355: contig of 6263 bp in length
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            *    16456    19763: contig of 3308 bp in length
            *    19764    19863: gap of unknown length
            *    19864    23522: contig of 3659 bp in length
            *    23523    23622: gap of unknown length
            *    23623    30934: contig of 7312 bp in length
            *    30935    31034: gap of unknown length
            *    31035    34928: contig of 3894 bp in length
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            *    35029    40294: contig of 5266 bp in length
            *    40295    40394: gap of unknown length
            *    40395    44738: contig of 4344 bp in length
            *    44739    44838: gap of unknown length
            *    44839    47425: contig of 2587 bp in length
            *    47426    47525: gap of unknown length
            *    47526    52087: contig of 4562 bp in length
            *    52088    52187: gap of unknown length
            *    52188    56217: contig of 4030 bp in length
            *    56218    56317: gap of unknown length
            *    56318    59654: contig of 3337 bp in length
            *    59655    59754: gap of unknown length
            *    59755    62837: contig of 3083 bp in length
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*    62838    62937: gap of unknown length
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*    66627    66726: gap of unknown length
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*    69750    69849: gap of unknown length
*    69850    73094: contig of 3245 bp in length
*    73095    73194: gap of unknown length
*    73195    76901: contig of 3707 bp in length
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*    77002    80609: contig of 3608 bp in length
*    80610    80709: gap of unknown length
*    80710    84410: contig of 3701 bp in length
*    84411    84510: gap of unknown length
*    84511    87179: contig of 2669 bp in length
*    87180    87279: gap of unknown length
*    87280    91311: contig of 4032 bp in length
*    91312    91411: gap of unknown length
*    91412    94760: contig of 3349 bp in length
*    94761    94860: gap of unknown length
*    94861    98682: contig of 3822 bp in length
*    98683    98782: gap of unknown length
*    98783   101453: contig of 2671 bp in length
*   101454   101553: gap of unknown length
*   101554   105675: contig of 4122 bp in length
*   105676   105775: gap of unknown length
*   105776   107767: contig of 1992 bp in length
*   107768   107867: gap of unknown length
*   107868   109988: contig of 2121 bp in length
*   109989   110088: gap of unknown length
*   110089   111632: contig of 1544 bp in length
*   111633   111732: gap of unknown length
*   111733   114165: contig of 2433 bp in length
*   114166   114265: gap of unknown length
*   114266   117015: contig of 2750 bp in length
*   117016   117115: gap of unknown length
*   117116   118975: contig of 1860 bp in length
*   118976   119075: gap of unknown length
*   119076   121573: contig of 2498 bp in length
*   121574   121673: gap of unknown length
*   121674   123805: contig of 2132 bp in length
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*   123906   126437: contig of 2532 bp in length
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*   126538   127750: contig of 1213 bp in length
*   127751   127850: gap of unknown length
*   127851   130560: contig of 2710 bp in length
*   130561   130660: gap of unknown length
*   130661   132488: contig of 1828 bp in length
*   132489   132588: gap of unknown length
*   132589   134250: contig of 1662 bp in length
*   134251   134350: gap of unknown length
*   134351   136751: contig of 2401 bp in length
*   136752   136851: gap of unknown length
*   136852   139762: contig of 2911 bp in length
*   139763   139862: gap of unknown length
*   139863   142157: contig of 2295 bp in length
*   142158   142257: gap of unknown length
*   142258   143334: contig of 1077 bp in length
*   143335   143434: gap of unknown length
*   143435   145117: contig of 1683 bp in length
*   145118   145217: gap of unknown length
*   145218   147349: contig of 2132 bp in length
*   147350   147449: gap of unknown length
*   147450   149137: contig of 1688 bp in length
*   149138   149237: gap of unknown length
*   149238   150932: contig of 1695 bp in length
*   150933   151032: gap of unknown length
*   151033   152519: contig of 1487 bp in length
*   152520   152619: gap of unknown length
*   152620   154047: contig of 1428 bp in length
*   154048   154147: gap of unknown length
*   154148   155596: contig of 1449 bp in length
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*   155697   157246: contig of 1550 bp in length
*   157247   157346: gap of unknown length
*   157347   158353: contig of 1007 bp in length
*   158354   158453: gap of unknown length
*   158454   159651: contig of 1198 bp in length
*   159652   159751: gap of unknown length
*   159752   161019: contig of 1268 bp in length
*   161020   161119: gap of unknown length
*   161120   162604: contig of 1485 bp in length
*   162605   162704: gap of unknown length
*   162705   163740: contig of 1036 bp in length
*   163741   163840: gap of unknown length
*   163841   165159: contig of 1319 bp in length
*   165160   165259: gap of unknown length

  Query Match             100.0%;  Score 15;  DB 2;  Length 170559;
  Best Local Similarity   100.0%;  Pred. No. 5.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCTGCTGAGG 15
           |||||||||||||||
Db   83978 GTCCGCCTGCTGAGG 83992


RESULT 12
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LOCUS       AB025351                 706 bp    mRNA    linear   VRT 03-AUG-2000
DEFINITION  Rana catesbeiana mRNA for BFCIRP, complete cds.
ACCESSION   AB025351
VERSION     AB025351.1  GI:6682988
KEYWORDS    BFCIRP.
SOURCE      Rana catesbeiana female liver cDNA to mRNA.
  ORGANISM  Rana catesbeiana
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
REFERENCE   1  (bases 1 to 706)
  AUTHORS   Saito,T., Sugimoto,K., Adachi,Y., Wu,Q. and Mori,K.J.
  TITLE     Cloning and characterization of amphibian cold inducible
            RNA-binding protein
  JOURNAL   Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 125 (2), 237-245
            (2000)
  MEDLINE   20362492
REFERENCE   2  (bases 1 to 706)
  AUTHORS   Sugimoto,K. and Saito,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-1999) Kenkichi Sugimoto, Niigata University,
            Faculty of Graduated School of Science and Technology; Igarashi
            Nino-cho 8050, Niigata, Niigata 950-2181, Japan
            (E-mail:sugimoto@sc.niigata-u.ac.jp, Tel:81-25-262-6151,
            Fax:81-25-262-6151)
FEATURES             Location/Qualifiers
     source          1. .706
                     /organism="Rana catesbeiana"
                     /db_xref="taxon:8400"
                     /sex="female"
                     /tissue_type="liver"
     CDS             58. .552
                     /codon_start=1
                     /product="BFCIRP"
                     /protein_id="BAA88978.1"
                     /db_xref="GI:6682989"
                     /translation="MSCDEGKLFVGGLSFDTDEQCLETVFSKYGQIQEVVVVKDRETK
                     RSRGFGFVTFENCEDAKDAMAGMNGKTVDGRQIRVDQAGKSSNDRRGGYRGGSSGGGR
                     GFFRGGRGRGGGGYGGSSRFDNRSGGGYGGWIPDYYSSGRESSYGDRSAGGRSYRDSY
                     DSYG"
BASE COUNT      175 a    125 c    228 g    178 t
ORIGIN

  Query Match             93.3%;  Score 14;  DB 5;  Length 706;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCCGCCTGCTGAG 14
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          ||||||||||||||
Db    517 GTCCGCCTGCTGAG 504


RESULT 13
A22950
LOCUS       A22950                 1100 bp    mRNA    linear   PAT 05-JUN-1995
DEFINITION  H.sapiens mRNA fragment (pRR14-35).
ACCESSION   A22950
VERSION     A22950.1  GI:1247418
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1100)
  AUTHORS   Franz,J., Weingaertner,B., Unterbeck,A. and Rae,P.
  TITLE     Calcium channel subtype specific of human neuronal tissue and its
            use
  JOURNAL   Patent: EP 0507170-A 17 07-OCT-1992;
            BAYER AG
FEATURES             Location/Qualifiers
     source          1. .1100
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      219 a    296 c    326 g    252 t      7 others
ORIGIN

  Query Match            93.3%;  Score 14;  DB 6;  Length 1100;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCGCCTGCTGAGG 15
          ||||||||||||||
Db    906 TCCGCCTGCTGAGG 919


RESULT 14
AR150761
LOCUS       AR150761               1100 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 17 from patent US 6229000.
ACCESSION   AR150761
VERSION     AR150761.1  GI:15115352
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1100)
  AUTHORS   Franz,J., Weingartner,B., Unterbeck,A. and Rae,P.
  TITLE     Tissue-specific human neuronal calcium channel subtypes and their
            use
  JOURNAL   Patent: US 6229000-A 17 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .1100
                     /organism="unknown"
BASE COUNT      219 a    295 c    322 g    252 t     12 others
ORIGIN

  Query Match            93.3%;  Score 14;  DB 6;  Length 1100;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCGCCTGCTGAGG 15
          ||||||||||||||
Db    906 TCCGCCTGCTGAGG 919


RESULT 15
I12881
LOCUS       I12881                 2470 bp    DNA     linear   PAT 26-JUL-1995
DEFINITION  Sequence 14 from patent US 5429921.
ACCESSION   I12881
VERSION     I12881.1  GI:910858
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2470)
  AUTHORS   Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F.
            and Brenner,R.
  TITLE     Assays for agonists and antagonists of recombinant human calcium
            channels
  JOURNAL   Patent: US 5429921-A 14 04-JUL-1995;
FEATURES             Location/Qualifiers
     source          1. .2470
                     /organism="unknown"
BASE COUNT      483 a    722 c    754 g    511 t
ORIGIN

  Query Match            93.3%;  Score 14;  DB 6;  Length 2470;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCGCCTGCTGAGG 15
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Db   1739 TCCGCCTGCTGAGG 1752


Search completed: November  2, 2002, 16:49:55
Job time : 325.727 secs
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